

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 : Search time 20.18 Seconds
(without alignments)
1102.527 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 1953
Sequence: 1 MKSKVLALIPALLAGAAH.....TRDAGINTDNLVALGLVYQF 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq.0601.*
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2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT.*
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21: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	98.0	367	20	AAV42549
2	1914	98.0	367	20	AAV34058
3	1914	98.0	367	21	AAV57356
4	1285	65.8	377	20	AAV34057
5	1285	65.8	377	21	AAV57355
6	1104	56.5	362	20	AAV42550
7	1078.5	55.2	323	20	AAV34056
8	1078.5	55.2	323	21	AAV57354
9	1027	52.6	340	17	AAW92998
10	226.5	11.6	89	18	AAW27781
11	187.5	9.6	353	20	AAV26025

12	176	9.0	362	10	AAV90098	P2 antigen of Haem
13	174	8.9	343	20	AAV26024	OMP protein of Pa
14	171	8.8	353	20	AAV26023	OMP protein of Pa
15	164.5	8.4	361	11	AAV05999	P2 gene product of
16	164.5	8.4	361	16	AAV66877	H. influenzae P2 e
17	161.5	8.3	390	18	AAV21678	Haemophilus influe
18	148.5	7.6	350	13	AAV27484	Protein IB. Synth
19	147.5	7.6	350	10	AAV90100	Class II outer mem
20	146	7.5	353	11	AAV06038	Class II outer mem
21	145.5	7.5	372	16	AAV69607	Class II outer mem
22	140.5	7.2	342	16	AAV70763	Mature class 2 por
23	140.5	7.2	342	18	AAV21742	Neisseria meningit
24	140.5	7.2	363	16	AAV70764	Fusion Class 2 por
25	140.5	7.2	363	18	AAV21743	Neisseria meningit
26	132	6.8	328	11	AAV06036	Class IB outer mem
27	130.5	6.7	341	11	AAV07043	P3 gene product of
28	128.5	6.6	589	20	AAV23745	A surface protein
29	127.5	6.5	326	11	AAV06037	Class IA outer mem
30	127.5	6.5	363	16	AAV66878	PNV-2 fusion const
31	127.5	6.5	373	11	AAV06043	Class I OMP derive
32	126.5	6.5	342	16	AAV66879	H. influenzae prot
33	126.5	6.5	342	16	AAV66880	H. influenzae prot
34	126.5	6.5	366	11	AAV06044	Class I OMP derive
35	125.5	6.4	373	14	AAV37328	Meningococcal p1.7
36	125	6.4	368	11	AAV06042	Meningococcal p1.7
37	124.5	6.4	341	11	AAV07042	Class I OMP derive
38	124.5	6.4	511	17	AAV95012	P3 gene product of
39	124.5	6.4	511	17	AAV95012	C. difficile toxin
40	124.5	6.4	608	17	AAV95013	C. difficile toxin
41	124.5	6.4	609	17	AAV95018	C. difficile toxin
42	124.5	6.4	611	17	AAV95012	C. difficile toxin
43	124.5	6.4	2366	17	AAV95011	C. difficile toxin
44	124.5	6.4	2366	19	AAV68388	Clostridium diffic
45	121	6.2	373	11	AAV06035	Class I outer mem

ALIGNMENTS

RESULT 1	AAV42549	standard; Protein; 367 AA.
ID	AAV42549	
AC	AAV42549	
XX		
DT	20-DEC-1999	(first entry)
XX		
DE	E. coli wild-type ompc protein.	
XX		
KW	Bacteria; attenuation; deletion; mutant; vaccine; immune response;	
KW	Gram negative; infection; diarrhoea; food poisoning; typhoid;	
KW	salmonellosis; gonorrhoea; gastroenteritis; whooping cough.	
XX		
OS	Escherichia coli.	
XX		
PN	WO949026-A1.	
XX		
PD	30-SEP-1999.	
XX		
PF	25-MAR-1999.	99WO-GB00935.
XX		
PR	25-MAR-1998.	98GB-0006449.
XX		
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.	
XX		
PI	Chatfield SN;	
XX		
DR	WPI; 1999-580447/49.	
XX		
DR	N-PSDB; AA222885.	
XX		
PT	New attenuated bacteria useful as vaccines for protecting against	
XX	infections	
XX		

PS Disclosure: Page 57-58; 69pp; English.

XX This sequence represents the *E. coli* wild-type ompC protein. The coding
 CC sequence of the ompC gene was removed via PCR using primers TT7-TT10
 CC (AA22883-22896) to produce a non-reverting deletion mutation. The
 CC mutant ompC gene (AA22886) was used in the production of a bacterium
 CC attenuated by a non-reverting mutation in each of the ompC gene, the *arcC*
 CC gene (AA22883), AA22884, and the *ompF* gene (AA22887, AA22888). The
 CC mutant bacteria provide immunogenic activity with reduced virulence and
 CC thus can be used as a vaccine for raising an immune response against a
 CC variety of bacteria in a mammalian host. Such vaccines can provide
 CC protection against e.g., *E. coli* (a cause of diarrhoea in humans),
 CC *Salmonella typhimurium* (the cause of salmonellosis in several animal
 CC species), *S. typhi* (the cause of human typhoid), *S. enteritidis* (a cause
 CC of food poisoning in humans), *S. choleraesuis* (a cause of salmonellosis
 CC in pigs), *S. dublin* (a cause of both a systemic and diarrhoeal disease in
 CC cattle, especially of new-born calves), *Haemophilus influenzae* (a cause
 CC of meningitis), *Neisseria gonorrhoeae* (a cause of gonorrhoea), *Yersinia*
 CC *enterocolitica* (the cause of a spectrum of disease in humans, ranging
 CC from gastroenteritis to fatal septicemic disease), *Bordetella pertussis*
 CC (the cause of whooping cough), and *Brucella abortus* (a cause of abortion
 CC and infertility in cattle and a condition known as undulant fever in
 CC humans).

XX Sequence 367 AA:

Query Match 98.0%; Score 1914; DB 20; Length 367;

Best Local Similarity 98.1%; Pred. No. 1.9e-145; Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MRSKVALLIPALLAAGAAHAAEVYKDKGKLDYGRVDGLHFSDNKDVGDQTYMRIG 60
 1 MKVKVLSIIPALLVAGANAEEVYKDKGKLDYGRVDGLHFSDNKDVGDQTYMRIG 60
 61 FKGETVDTQLTGCGMEYQIQGNSAENENNSWTRVAFAGLKRQDVGSFQGRNRYVD 120
 61 FKGELTVDTQLTGCGMEYQIQGNSAENENNSWTRVAFAGLKRQDVGSFQGRNRYVD 120
 121 VTSMTDVLPEFGGDTYGSNFMQGRNFGATYRNTDFGLVDGLNFAVOYQKGNPSE 180
 121 VTSMTDVLPEFGGDTYGSNFMQGRNFGATYRNTDFGLVDGLNFAVOYQKGNPSE 180
 181 GFTSGTNNRDLRONGGVGSGITDYDEGFGIGAISSSKRTDAQNTAATYTGNDRAE 240
 181 GFTSGTNNRDLRONGGVGSGITDYDEGFGIGAISSSKRTDAQNTAATYTGNDRAE 240
 241 TTTGGLKYDANNIYLAAYTOTYNNATRVGSLGANKAQNFEAVAOYQFQGRPSLAYIQ 300
 241 TTTGGLKYDANNIYLAAYTOTYNNATRVGSLGANKAQNFEAVAOYQFQGRPSLAYIQ 300
 301 SKGKNLGRGYDDEDLIKYDVAGATYFNKNMSTYVDYKINLDDNQFTDAGINTDNIYA 360
 301 SKGKNLGRGYDDEDLIKYDVAGATYFNKNMSTYVDYKINLDDNQFTDAGINTDNIYA 360
 361 LGIVYQF 367
 361 LGIVYQF 367

RESULT 2

AAV34058 standard; protein; 367 AA.

AAV34058;

23-NOV-1999 (first entry)

E. coli outer membrane protein c precursor.

Ulcerative colitis; histone; H1-like antigen; porin antigen;
 Bacteroides antigen; IBD; PANCA; inflammatory bowel disease;
 diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;

KW outer membrane protein c precursor.

OS Escherichia coli.

PN MO9945955-A1.

PD 16-SEP-1999.

PF 12-MAR-1999; 99WO-US05492.

PR 12-MAR-1998; 98US-0041889.

PA (REGC) UNIV CALIFORNIA.

PI Braun J, Cohavy O;

DR WPI; 1999-55125/46.

PT Use of histone H1, porin or Bacteroides antigens as targets for the
 PT diagnosis, prevention and treatment of ulcerative colitis

PS Claim 8; Fig 11; 134pp; English.

The invention provides a method for the diagnosis, prevention and
 treatment of ulcerative colitis (UC) using histone H1-like antigen, a
 porin antigen or a Bacteroides antigen as a target antigen. The novel
 method of diagnosing UC in a subject suspected of having inflammatory
 bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
 (2) contacting the sample with a histone H1-like antigen, or perinuclear
 anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a
 complex of the histone H1-like antigen, or the PANCA-reactive fragment,
 and antibody to the histone H1-like antigen; and (3) detecting the
 presence or absence of the complex; where the presence of the complex
 indicates that the subject has UC. The PANCA-reactive histone H1-like
 antigen, porin antigen and Bacteroides antigen are useful in the
 diagnosis, prevention and treatment of UC. The methods can also be used
 for identifying agents useful for treating UC. The present sequence
 represents a *E. coli* outer membrane protein c precursor.

XX Sequence 367 AA:

Query Match 98.0%; Score 1914; DB 20; Length 367;

Best Local Similarity 98.1%; Pred. No. 1.9e-145; Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MRSKVALLIPALLAAGAAHAAEVYKDKGKLDYGRVDGLHFSDNKDVGDQTYMRIG 60
 1 MKVKVLSIIPALLVAGANAEEVYKDKGKLDYGRVDGLHFSDNKDVGDQTYMRIG 60
 61 FKGETVDTQLTGCGMEYQIQGNSAENENNSWTRVAFAGLKRQDVGSFQGRNRYVD 120
 61 FKGELTVDTQLTGCGMEYQIQGNSAENENNSWTRVAFAGLKRQDVGSFQGRNRYVD 120
 121 VTSMTDVLPEFGGDTYGSNFMQGRNFGATYRNTDFGLVDGLNFAVOYQKGNPSE 180
 121 VTSMTDVLPEFGGDTYGSNFMQGRNFGATYRNTDFGLVDGLNFAVOYQKGNPSE 180
 181 GFTSGTNNRDLRONGGVGSGITDYDEGFGIGAISSSKRTDAQNTAATYTGNDRAE 240
 181 GFTSGTNNRDLRONGGVGSGITDYDEGFGIGAISSSKRTDAQNTAATYTGNDRAE 240
 241 TTTGGLKYDANNIYLAAYTOTYNNATRVGSLGANKAQNFEAVAOYQFQGRPSLAYIQ 300
 241 TTTGGLKYDANNIYLAAYTOTYNNATRVGSLGANKAQNFEAVAOYQFQGRPSLAYIQ 300
 301 SKGKNLGRGYDDEDLIKYDVAGATYFNKNMSTYVDYKINLDDNQFTDAGINTDNIYA 360
 301 SKGKNLGRGYDDEDLIKYDVAGATYFNKNMSTYVDYKINLDDNQFTDAGINTDNIYA 360
 361 LGIVYQF 367
 361 LGIVYQF 367

```

RESULT 3
AAV57356
ID AAV57356 standard: protein; 367 AA.
XX
XX AAV57356;
AC
XX
XX 13-JUN-2000 (first entry)
XX
XX
DE E. coli outer membrane protein c precursor.
XX
XX Ulcerative colitis; inflammatory bowel disease; porin antigen; Mab;
XX PANCA; perinuclear anti-neutrophil cytoplasmic antibody;
XX histone H1; outer membrane protein c precursor.
XX
XX Escherichia coli.
XX
XX US6033864-A.
XX
XX 07-MAR-2000.
XX
XX 12-MAR-1998; 98US-0041889.
XX
XX 12-APR-1996; 96US-0057846.
XX
XX 11-APR-1997; 97US-0837058.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Cohavy O, Braun J;
XX
XX WPI; 2000-255695/22.
XX
XX
XX Diagnosing ulcerative colitis or susceptibility, by detecting complex
XX formation between microbial porin antigen and perinuclear
XX anti-neutrophil cytoplasmic autoantibodies
XX
XX Claim 1; Fig 10; 49pp; English.
XX
XX The invention provides a method for diagnosing ulcerative colitis in a
XX subject suspected of having inflammatory bowel disease. The method
XX comprises reacting a patient sample with a porin antigen that is
XX immunologically reactive with PANCA (perinuclear anti-neutrophil
XX cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex
XX as indicative of ulcerative colitis. The method is used to diagnose
XX ulcerative colitis or susceptibility to it. The present sequence
XX represents a E. coli outer membrane protein c precursor.
XX
XX
XX Sequence 367 AA:
SQ
Query Match 98.0%; Score 1914; DB 21; Length 367;
Best Local Similarity 98.1%; Pred. No. 1,9e-145;
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 MRSKVALLIPALLAAGAAHAAYNNKDKNKLIDYGVKVDGLHYFSDNKKVDQDTYMRG 60
DB 1 MKVKVLSILVPLLIVAGAAAEVYNNKDKNKLIDYGVKVDGLHYFSDNKKVDQDTYMRG 60
OY 61 FGEIYQVTDQLTGIGYOMEQIOGNSAENNNNSWTRAFGLKFDYGSDDYGRNTGVYD 120
DB 61 fkeqbtvtqlgygyqweyqignsaenennswtrvafglkfgydgsfdygrnygvvyd 120
OY 121 VTSWTDVLPEFGGDYNGSNFMQORNGNFCATYRNTDFGLVGLNPAVOYOGKNGNPSGE 180
DB 121 vtswtdvlpefsgdyngsgnfmqorngnfcaty rntdfglv gln pavo yogkngnpsge 180
OY 181 GFTSGVTNNGRDALRQNGDVGSGSTIYDEGFGIGALSSSKRTDAQONTAAVIGNGDRAE 240
DB 181 gftsgvt nng rdal r qng dvg sg st i y de g fg i ga l ss sk rt da q on t aa v i g ng d r ae 240
OY 241 YTTGGGKRYANNITTLAAQYTOTYNNATRVGSLGMANKAQQFEAVAOYQPFGLRPSLAVYQ 300
DB 241 yttgggkryannit t l a a q y t o t y n n a t r v g s l g m a n k a q q f e a v a o y q p f g l r p s l a v y q 300

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DB 241 tytgglkydaanniyaaqytlqtnatrvyslgwankagnfeavagqyfdqrlrpslavlq 300
OY 301 SKGKNLGRGVDEDEDLKYVDVGCATYFFNNKMSTYYDYKINLLDNOFFRDAGINTDNIVA 360
DB 301 skgknlgrgvdededllkyvdv gcat yff n n k m s t y y d y k i n l l d n o f f r d a g i n t d n i v a 360
OY 361 IGLVYQF 367
DB 361 lglvyqf 367
RESULT 4
AAV34057
ID AAV34057 standard: protein; 377 AA.
XX
XX AAV34057;
AC
XX
XX 23-NOV-1999 (first entry)
XX
XX
DE E. coli outer membrane protein F precursor.
XX
XX Ulcerative colitis; histone; H1-like antigen; porin antigen;
XX Bacteroides antigen; IBD; PANCA; inflammatory bowel disease;
XX diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;
XX outer membrane protein F precursor.
XX
XX Escherichia coli.
XX
XX WO9945955-A1.
XX
XX 16-SEP-1999.
XX
XX 12-MAR-1999; 99WO-US05492.
XX
XX 12-MAR-1998; 98US-0041889.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Braun J, Cohavy O;
XX
XX WPI; 1999-551215/46.
XX
XX
XX Use of histone H1, porin or Bacteroides antigens as targets for the
XX diagnosis, prevention and treatment of ulcerative colitis
XX
XX Claim 8; Fig 11; 134pp; English.
XX
XX The invention provides a method for the diagnosis, prevention and
XX treatment of ulcerative colitis (UC) using histone H1-like antigen, a
XX porin antigen or a Bacteroides antigen as a target antigen. The novel
XX method of diagnosing UC in a subject suspected of having inflammatory
XX bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
XX (2) contacting the sample with a histone H1-like antigen, or perinuclear
XX anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a
XX complex of the histone H1-like antigen, or the PANCA-reactive fragment,
XX and antibody to the histone H1-like antigen; and (3) detecting the
XX presence or absence of the complex; where the presence of the complex
XX indicates that the subject has UC. The PANCA-reactive histone H1-like
XX antigen, porin antigen and Bacteroides antigen are useful in the
XX diagnosis, prevention and treatment of UC. The methods can also be used
XX for identifying agents useful for treating UC. The present sequence
XX represents a E. coli outer membrane protein F precursor.
XX
XX
XX Sequence 377 AA:
SQ
Query Match 65.8%; Score 1285; DB 20; Length 377;
Best Local Similarity 67.3%; Pred. No. 4.5e-95;
Matches 259; Conservative 38; Mismatches 62; Indels 26; Gaps 10;
OY 1 MRSKVALLIPALLAAGAAHAAYNNKDKNKLIDYGVKVDGLHYFSDNKKVDQDTYMRG 60
DB 1 mskviall i p a l l a a g a a h a a e v n n k d k n k l i d y g v k v d g l h y f s d n k k v d q d t y m r g 60

```


DT 13-JUN-2000 (first entry)
 XX E. coli outer membrane protein F precursor.
 DE
 XX
 XX
 KM ulcerative colitis; inflammatory bowel disease; porin antigen; Mab;
 KM PANCA; perinuclear anti-neutrophil cytoplasmic antibody;
 KM histone H1; outer membrane protein F precursor.
 XX
 OS Escherichia coli.
 XX
 PN US6033864-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 12-MAR-1998; 98US-0041889.
 XX
 PR 12-APR-1996; 96US-0057846.
 PR 11-APR-1997; 97US-0837058.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Cohavy O, Braun J;
 PI
 DR WPI; 2000-255695/22.
 XX
 XX Diagnosing ulcerative colitis or susceptibility, by detecting complex
 PT formation between microbial porin antigen and perinuclear
 PT anti-neutrophil cytoplasmic autoantibodies -
 XX
 PS Claim 1, Fig 10; 49pp: English.
 XX
 CC The invention provides a method for diagnosing ulcerative colitis in a
 CC subject suspected of having inflammatory bowel disease. The method
 CC comprises reacting a patient sample with a porin antigen that is
 CC immunologically reactive with PANCA (perinuclear anti-neutrophil
 CC cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex
 CC as indicative of ulcerative colitis. The method is used to diagnose
 CC ulcerative colitis or susceptibility to it. The present sequence
 CC represents a E. coli outer membrane protein F precursor.
 XX
 XX
 SQ Sequence 323 AA;

Query Match 55.2%; Score 1078.5; DB 21; Length 323;
 Best Local Similarity 66.2%; Pred. No. 1.2e-78;
 Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps 9;

QY 1 MKSKVIALILPALAAGAAHAAEVYKNDGKLDLYGKVDGLHFSDNKDYDGGQTYMRIG 60
 |||
 DB 1 mkskvialilpalaaagaaevynkdkldlygkvdglhfyfshsaksdqysariq 60
 |||
 QY 61 FKGETVTDQLTYGQWEOYIOGNSAE-NENNSWTRVAFAGLKFEODVGSFDRNGVYV 119
 |||
 DB 61 fkegetvtdqltygqeweyoiognsae-nennswtrvafaglkfeyodvgsfdrnrvyvy 120
 |||
 QY 120 DVTSMWTDVLPREFGDTY-GSDNFMQORNGFNATRYRTDFEGLVDGLNFAVOYOGKNGNPS 178
 |||
 DB 120 dvtswtdvlprefgdtv-gsdnfmqorngfnatryrtdfeglvdglnfavooyogkngnps 178
 |||
 QY 121 dtegwtdmpefgydsytnadnfmctgrangvalyrtndffglvnglnfavgysgn- 176
 |||
 DB 121 dtegwtdmpefgydsytnadnfmctgrangvalyrtndffglvnglnfavgysgn- 176
 |||
 QY 179 GEGFTYGV--TNNGRDALRONGDVGSGSTYDY-BEGFGIGALSSSKRTDAQ--NTAAAT 233
 |||
 DB 179 gegfthygv--tnngrdalrongdvsgsgsttydy-begfgigalssskrtdaq--ntaati 233
 |||
 QY 234 GNDRAETVYTGGLKYDANNIYLAQYTOTNATRVGSLGW--ANKAQNFEAVAYQOFDFG 291
 |||
 DB 234 gndraetvtytgglkydanniylaqytotnatrvvgslgw--ankaqnfeavayqofdfg 291
 |||
 QY 292 LRPSLAYLQSKGNL-----GRGYDDED 314
 |||
 DB 292 lrpslaylqskgnl-----grgydded 314
 |||
 DB 293 lrpavsfimskgrdlhaagadnagvddkd 323

RESULT 9

AAW92998
 ID AAW92998 standard; protein; 340 AA.
 XX
 AC AAW92998;
 XX
 DT 19-MAY-1999 (first entry)
 XX
 DE E. coli OmpF porin protein.
 XX
 KM OmpF; porin; amphiphilic alpha-structure; beta-structure; GLUT;
 KM membrane protein; glucose transporter protein; function.
 XX
 OS Escherichia coli.
 XX
 PN WO9618957-A1.
 XX
 PD 20-JUN-1996.
 XX
 PF 13-DEC-1995; 95WO-US16126.
 XX
 PR 14-DEC-1994; 94US-0355844.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Cheung M, Czegledy F, Fischberg J, Iserovich P;
 PI Li J;
 DR WPI; 1996-300839/30.
 XX
 XX Predicting tendency to form amphiphilic alpha and beta structures -
 PT using a novel algorithm to calculate values for subsequent graphical
 PT analysis to predict protein structure
 XX
 PS Disclosure; Fig 2; 106pp: English.
 XX
 CC This invention describes a novel method for predicting the tendency of
 CC a protein to form either: (a) an amphiphilic alpha-structure or (b) an
 CC amphiphilic beta-structure. The methods are used particularly for
 CC predicting the structure of membrane proteins such as glucose transporter
 CC proteins (GLUTs). They can be used to discern the function of proteins.
 CC They can also be used for the rational design or identification of
 CC compounds which interact with the proteins or to engineer proteins having
 CC particular structures. This sequence represents an Escherichia coli
 CC OmpF porin which is used to illustrate the method of the invention.
 XX
 XX
 SQ Sequence 340 AA;

Query Match 52.6%; Score 1027; DB 17; Length 340;
 Best Local Similarity 58.4%; Pred. No. 1.8e-74;
 Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

QY 22 AEVYKNDGKLDLYGKVDGLHFS-----DNKDVDSDQTYMRIGFEGQVTDQLTYGQ 76
 |||
 DB 22 aevyknkdkldlygkvdglhfs-----dnkdvdqdqtymrifegqvtdqltygq 76
 |||
 QY 77 WEYOIGNSAEN---ENNSWTRVAFAGLKFEODVGSFDRNGVYDVTSMWTDVLPREFG 133
 |||
 DB 77 weyoignsaen---ennswtrvafaglkfeyodvgsfdrnrvydyvtswtdvlprefg 133
 |||
 QY 134 DTYGSDNFMQORNGFNATRYRTDFEGLVDGLNFAVOYOGKNGNPSGEGFTSCVTNNGRD- 192
 |||
 DB 134 dtygsdnfmqorngfnatryrtndfeglvdglnfavooyogkngnpsgegftscvtnngrd- 192
 |||
 QY 193 ALRONGDVGSGSTYVBEFGIGALSSSKRTDAQNTAAATYIGNDRAETVYTGGLKYDANN 252
 |||
 DB 193 alrongdvsgsgsttyvbefgigalssskrtdaqntaatiyigndraetvtytgglkydanni 252
 |||
 QY 253 IYLAQYTOTNATRV-----GSLGWANKAQNFEAVAYQOFDFGLRPSLAYLQSKGNL 307
 |||
 DB 253 iylaqytotnatrv-----gslgwankaqnfeavayqofdfglrpslaylqskgnl 307
 |||
 DB 225 iylaanygetnatpntkftntsfanktqdvllvagqydfglrpslaylqskakdv- 283
 |||
 QY 308 RGYDDEDILKYVDVGAATYTFNKNMSTYVDYKINLND-DNQPTRDAGINTDNVALGLVYQ 366
 |||

03 STIMULATING

```

QY      81  IGSNSENNSMTWVAFAGLKEFQDVGSPDYGRNRYGVVDTSWTDLPEFGDPTGSDN 140
      108  -----tklayaglnkeibeatfgtqktadistred--keyg--vikns 150
QY      141  FMOQRG-----FGATY---RNTDFEGLVDG-LNFAYOYQK-NGNPSGEG 181
      151  yipegnaiaytykgleglitgaayvfgrnfsdgyeltdgkvsnavgvakkydanniavag 210
QY      182  FTSQVTN-NQRDALRQGDVGSIITYDIEGFGT-----GGAISSKRTDAQNTAAITGN 235
      211  faysrtlnykgagqaktgvgngalatlyghfdlglilslsdgyaktknkadekhekyrtvsp 270
QY      236  GDRAE-----TYTGELKYDANNIYLAQYQTYNATRVGSLGMANKAQNFEAVAOYOFDE 290
      271  gfgyelmednlygnlkyer-----insvdgqekvrehavlf 307
Db
QY      291  GLRPSL-----AYLOSCKNLRGVDDEDILKYVDVGYATYF 327
      308  gidhklhkqylylegayartndkgtktek-eksvvgjrlvyf 353

```

RESULT 12

```

AAP90098
ID  AAP90098 standard; protein; 362 AA.
XX
AC  AAP90098;
XX
DT  01-NOV-1989 (first entry)
XX
DE  P2 antigen of Haemophilus influenzae.
XX
KW  Haemophilus influenzae P2 antigen; vaccines; pathogenic
   type b strains.
XX
OS  Haemophilus influenzae type b.
XX
PN  EP320289-A.
PD  14-JUN-1989.
XX
PF  09-DEC-1988; 88EP-0311691.
XX
PR  10-DEC-1987; 87US-0249482.
XX
PA  (TEXA ) UNIV OF TEXAS SYST.
XX
PI  Hansen EJ;
XX
DR  WPI; 1989-174562/24.
XX
PT  DNA encoding Haemophilus influenzae P2 antigen
   used for producing immunogenic comps. as vaccines
   and in diagnostic hybridisation assays.
XX
PS  Disclosure; fig 6; 20pp; English.
XX
CC  P2 antigen of Haemophilus influenzae (see corresp. AAN90033).
CC  Isolated from type b strains, the P2 antigens are used as vaccines
CC  and to detect P2-specific RNA or DNA. Segments used as antigens
CC  include amino acids 21-361, 175-197, 260-275, 296-311, 33-353,
CC  or their functional equivalents.
XX
SQ  Sequence 362 AA;

```

Query Match 9.0%; Score 176; DB 10; Length 362;
 Best Local Similarity 24.1%; Pred. No. 2.5e-06;
 Matches 90; Conservative 53; Mismatches 145; Indels 86; Gaps 16;

```

QY      4  KVALALIPALLAAGAAAEVYNNKDKMLDYGKVDGLHFSNKNKDVDDQTY----- 56
      3  ktlaailivgaafaasanaavvynnegunvelggrlsliaeqsnstvdkqghgalnrg 62

```

```

QY      57  -MRLEKGETQVITDOLITGCGWEXYLOGNSAENENNSM-----TRVAFAGLKEFQDVGSEFDY 111
      63  gsrflhkatnfdggyaagyljetrfvtksengschfdgtstkyvyltgnkafgevrk 122
QY      112  GRNRYGVVDTSWTDLPEFGDPTGSDNPMQQRG-NFGATYRNTDFEGLVDGLNFAVOY 170
      123  graktladgitsaed--keyg--vlnmsdyipcsnhtvgytftkgid--glvlgany----- 172
QY      171  QKNGNNGSGSGFNSGVYNNRDLARQGDVGSIITYDIEGFGTGGGAISSKRTDAQNTA 230
      173  -----llaqkregakg-----enkrpndkage 194
QY      231  AYIG---NGDRAETTYGELKYDANNIYLAQYQTYT---YNATRVGSLGMANKAO--NFEA 282
      195  vrlgelngiqv-----gakydandilvaklaygrtnykyhesd-----ehkqglngvla 243
QY      283  VAOYQF-DFGLRPSLAYLOSCKNLRGVDDEDILKYVDVGYATYFNNKNSYVDYKI-- 339
      244  tlgyrtfdlglilslsdgyaktknkylkhekr--yfvspgfygelmednlygnfkkyer 300
Db
QY      340  NILDDNQFTRDAGI 353
      301  tsvdgqektregev 314

```

RESULT 13

```

AAY26024
ID  AAY26024 standard; protein; 343 AA.
XX
AC  AAY26024;
XX
DT  29-SEP-1999 (first entry)
XX
DE  OmpH protein of Pasteurella multocida P-1059.
XX
KW  Outer membrane protein H; ompH gene; fowl cholera; molecular sieve;
   Pasteurella multocida P-1059; porin; vaccine; veterinary medicine;
   bacterial porin; H.influenzae porin P2; avian.
XX
OS  Pasteurella multocida.
XX
FH  Key
FT  Peptide
   Location/Qualifiers
   1..20
   /label= "Signal_peptide"
   /note= "Hydrophobic amino acids"
   21..343
   /note= "mature OmpH protein"
FT  Cleavage-site
   7..9
   /note= "Found within signal peptide"
FT  Cleavage-site
   9..11
   /note= "Found within signal peptide"
FT  Cleavage-site
   12..14
   /note= "Found within signal peptide"
FT  Cleavage-site
   18..20
   /note= "Found within signal peptide"
XX
XX  WO92929724-A2.
XX  PN
XX  17-JUN-1999.
XX  PD
XX  PF  08-DEC-1998; 98WO-US25990.
XX  PR  21-JUL-1998; 98US-0120051.
XX  PR  08-DEC-1997; 97US-0067957.
XX  PA  (UYGE-) UNIV GEORGIA RES FOUND INC.
XX  PI  Glisson JR, Luo Y;
XX  DR  WPI; 1999-385575/32.
XX  DR  N-PSDB; AAX80610.
XX  PT  DNA encoding Pasteurella multocida outer membrane protein H, useful

```



```

QY 99 AGLKFDVGSFDDYGRNRYVYDTSWTVDLPEFGDPTYSNDNMQKNGKATYRNTDF 158
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 agfayeglgltlgnqlt-----gddvnglsdy-----ty----- 144
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 159 GLVDGLNFAVOYOGKNGNPSGEFTSGVTNNGRDALRONGDVGSGSTTYDEFGIGAI 218
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 -----fnglgn-----llsgekalnfksaefngftfgay 176
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 SSSKRDDAQNFAVIGNGDRAEYTGGL---KTDANNIYLAOYTOTY-----NATRV 268
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 vfa--ddadqalrldgrg---fvaaglynrkmgdvgafeagysqkyvqveqnpaa 230
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 269 GSGGNANKAQNFEAVAOYDFGLRPSLAYLQSKGN-----LGRGYDDEDILK-Y 318
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 qkvfkdekeaklmvgaelsy-aglaigvdyagskvtvdgkralavglnydlndrakvy 289
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 319 VD-----VGATYYFNKNMSTYYDYKINLDDNQFTRDAGINT-DNI 358
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 290 tdfiwekeqpgdvtrnrtvaavgfygylhkqvelfveaaggrekdsd-----gvtckny 344
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 359 VALGLVYQF 367
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 vgtglrvhf 353
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
AAR05999
ID AAR05999 standard; protein; 361 AA.
XX
AC AAR05999;
XX
DT 04-DEC-1990 (first entry)
XX
DE P2 gene product of Haemophilus strain 1H.
XX
KW P2 gene; strain 1H; Influenza; vaccine; ds.
XX
OS Haemophilus influenzae.
XX
PN EP378929-A.
XX
PD 25-JUL-1990.
XX
PF 22-DEC-1989; 89EP-0313573.
XX
PR 01-FEB-1989; 89GB-0002178.
XX
PR 23-DEC-1988; 88GB-0030124.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Munson RS, Tolan RW, Chong P, Fahlm R, Mcverry P, Klein M;
XX
DR WPI; 1990-225607/30.
XX
DR N-PSDB; AA005372.
XX
PT Gene coding for protein P2 of Haemophilus influenzae type-B -
PT used for developing vaccines for protection against disease
PT caused by the organism.
XX
PS Claim 1; Page 8; 15pp; English.
XX
CC Peptide may be used as a vaccine to the disease caused by H1
CC type b, as carrier for conjugation to oligosaccharide derived
CC from Haemophilus. Protein may be used with other haptens as
CC T-cell dependant antigen and carrier.
XX
SQ Sequence 361 AA;

```

Query Match 8.4%; Score 164.5; DB 11; Length 361;
 Best Local Similarity 24.1%; Pred. No. 2.1e-05;
 Matches 90; Conservative 52; Mismatches 145; Indels 87; Gaps 17;

```

QY 4 KVIALILPALLAGAAHAAEVYKKDGNKLDLYGKYVDGLHFSDNKNKVDGQTY----- 56
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 ktlaaalivgafaasanaaavvynneglnvelggrlslaeqs-nstvdnqkqhgallng 61
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 -MRLGKGEQVVDQLTGYGOWEYQIOGNSAENENNSW---TRVAFAGLKFDVGSFPDY 111
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 gsrfhkathnfgdgyaqgyletrfvtkasengsnfdltskayvclgnkafgevkl 121
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 112 GRNRYVYDTSWTVDLPEFGDPTYSNDNMQKNGN-FCATYRNTDFGLVDGLNFAVOR 170
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 graaktladgitsaed--keyg--vlnsdyipltsghvtytfkglid--glvlgany---- 171
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 QGKNGNPSGEGFTSGVTNNGRDALRONGDVGSGSTTYDEFGIGAISSSKRTRDAQNTA 230
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 -----llaqkregakg-----enkrpndkage 193
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 231 AYIG---NGDRAETTYGGLKYDANNIYLAOYTOT---YNATRVGSLGNANKAQ--NFEA 282
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 vrigelnglqv-----gakkydandlvaklaygrtnykynead-----ehkqqlngvla 242
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 283 VAOYQF-DFGLRPSLAYLQSKGNLGRGYDDEDILKYVDVGATYYFNKNMSTYYDYKI-- 339
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 flgyrfsdglivslidsyayaktnykhkhr---yfvspgfyglmedtnvygnfkkyer 299
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 340 NLLDDNQFTRDAGI 353
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 tsydggektregav 313
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: September 25, 2001, 15:53:50
 Job time: 29 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 : Search time 12.29 seconds
(without alignments)
614,862 Million cell updates/sec

Title: US-09-575-061-1

Sequence: 1 MKSKVLALLPALAAGAAH.....TRDAGINTDITVALGLVYQF 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	98.0	367	3	US-09-041-889-30
2	1285	65.8	377	3	US-09-041-889-29
3	1078.5	55.2	323	3	US-09-041-889-28
4	1027	52.6	340	2	US-08-355-844-1
5	1027	52.6	340	5	PCT-US95-16126-1
6	164.5	8.4	361	4	US-08-096-181A-8
7	164.5	8.4	361	5	PCT-US94-08326-8
8	140.5	7.2	342	1	US-08-096-182A-4
9	140.5	7.2	342	1	US-08-877-109-4
10	140.5	7.2	342	3	US-08-798-760-4
11	140.5	7.2	342	5	PCT-US94-08327-4
12	140.5	7.2	363	1	US-08-096-182A-6
13	140.5	7.2	363	1	US-08-877-109-6
14	140.5	7.2	363	3	US-08-798-760-6
15	140.5	7.2	363	5	PCT-US94-08327-6
16	128.5	6.6	589	4	US-09-377-155-19
17	127.5	6.5	363	4	US-08-096-181A-10
18	127.5	6.5	363	5	PCT-US94-08326-10
19	126.5	6.5	342	4	US-08-096-181A-12
20	126.5	6.5	342	4	US-08-096-181A-14
21	126.5	6.5	342	5	PCT-US94-08326-12
22	124.5	6.4	511	1	US-08-480-604A-20
23	124.5	6.4	511	2	US-08-480-604A-21
24	124.5	6.4	608	1	US-08-405-496A-20
25	124.5	6.4	608	2	US-08-405-496A-21
26	124.5	6.4	608	2	US-08-405-496A-21
27	124.5	6.4	609	1	US-08-480-604A-30

28	124.5	6.4	2366	1	US-08-480-604A-10	Sequence 10, Appl
29	124.5	6.4	2366	2	US-08-405-496A-10	Sequence 10, Appl
30	118.5	6.1	309	1	US-08-096-182A-2	Sequence 2, Appl
31	118.5	6.1	309	1	US-08-877-109-2	Sequence 2, Appl
32	118.5	6.1	309	3	US-08-798-760-2	Sequence 2, Appl
33	118.5	6.1	309	5	PCT-US94-08327-2	Sequence 2, Appl
34	116.5	6.0	598	4	US-09-377-155-5	Sequence 5, Appl
35	116.5	5.8	592	4	US-09-377-155-17	Sequence 17, Appl
36	113.5	5.8	599	4	US-09-377-155-15	Sequence 15, Appl
37	112.5	5.8	594	4	US-09-377-155-7	Sequence 7, Appl
38	112.5	5.8	1657	3	US-09-057-570-2	Sequence 7, Appl
39	112.5	5.8	1805	3	US-09-057-570-7	Sequence 7, Appl
40	111.5	5.7	598	4	US-09-377-155-13	Sequence 13, Appl
41	111	5.7	3031	1	US-07-689-008-2	Sequence 2, Appl
42	110.5	5.7	591	4	US-09-377-155-11	Sequence 11, Appl
43	110.5	5.7	591	4	US-09-377-155-21	Sequence 21, Appl
44	110.5	5.7	592	4	US-09-377-155-2	Sequence 2, Appl
45	110	5.6	341	2	US-08-538-711A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-041-889-30
; Sequence 30, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes thereof, Using
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-041-889-30

Query Match 98.0%; Score 1914; DB 3; Length 367;
Best Local Similarity 98.1%; Pred. No. 1,4e-157;
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MRSKVALLIPALLAAGAAHAAEYNNKDGKLDLYGKVDGLHFSDNKKVDGQDTYMRLG 60
Db 1 MKVYVLSLVPALLVAGAAHAAEYNNKDGKLDLYGKVDGLHFSDNKKVDGQDTYMRLG 60
QY 61 FKGTQVTDLTGTGQWEYIOGSAENENNSWTRVAFAGLKFDVGSFDYGRNRYGVYD 120
Db 61 FKGTQVTDLTGTGQWEYIOGSAENENNSWTRVAFAGLKFDVGSFDYGRNRYGVYD 120
QY 121 VTSWTDVLPFEGGDTYSGDNFMQGRNGFATYRTDFEGLVDGLNFAYOYQKGNFSGE 180
Db 121 VTSWTDVLPFEGGDTYSGDNFMQGRNGFATYRTDFEGLVDGLNFAYOYQKGNFSGE 180
QY 181 GFSTGVYNNGRDALRQNGDVGSGITVDYEGFGIGAISSSKRTDAONTAAYTGNGDRAE 240
Db 181 GFSTGVYNNGRDALRQNGDVGSGITVDYEGFGIGAISSSKRTDAONTAAYTGNGDRAE 240
QY 241 TYTGGLKYDANNITYLAQYOTYNATRVGSLGANKQNEEVAQYQFDEGLRPSLAYLQ 300
Db 241 TYTGGLKYDANNITYLAQYOTYNATRVGSLGANKQNEEVAQYQFDEGLRPSLAYLQ 300
QY 301 SKGNLGRGYDEDEILKYVDVGAATYFNKNMSTYVDYKINLDDNCFTRDAGINTDNIYA 360
Db 301 SKGNLGRGYDEDEILKYVDVGAATYFNKNMSTYVDYKINLDDNCFTRDAGINTDNIYA 360
QY 361 LGLVYQF 367
Db 361 LGLVYQF 367

```

RESULT 2

US-09-041-889-29

Sequence 29, Application US/09041889

Patent No. 6033864

GENERAL INFORMATION:

APPLICANT: Braun, Jonathan

APPLICANT: Conavy, Ofer

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, using

TITLE OF INVENTION: Microbial UC PANCA antigens

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,889

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/837,058

FILING DATE: 11-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-PM 3006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 377 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-041-889-29

Query Match 65.8%; Score 1285; DB 3; Length 377;
 Best Local Similarity 67.3%; Pred. No. 2,8e-103;
 Matches 259; Conservative 38; Mismatches 62; Indels 26; Gaps 10;

```

QY 1 MRSKVALLIPALLAAGAAHAAEYNNKDGKLDLYGKVDGLHFSDNKKVDGQDTYMRLG 60
Db 1 MKSVALLIPALLAAGAAHAAEYNNKDGKLDLYGKVDGLHFSDNKKVDGQDTYMRLG 60
QY 61 FKGTQVTDLTGTGQWEYIOGSAE--NENNSWTRVAFAGLKFDVGSFDYGRNRYGVY 119
Db 61 FKGTQVTDLTGTGQWEYIOGSAE--NENNSWTRVAFAGLKFDVGSFDYGRNRYGVY 119
QY 121 VTSWTDVLPFEGGDTYSGDNFMQGRNGFATYRTDFEGLVDGLNFAYOYQKGNFSGE 180
Db 121 VTSWTDVLPFEGGDTYSGDNFMQGRNGFATYRTDFEGLVDGLNFAYOYQKGNFSGE 180
QY 181 GFSTGVYNNGRDALRQNGDVGSGITVDYEGFGIGAISSSKRTDAONTAAYTGNGDRAE 240
Db 181 GFSTGVYNNGRDALRQNGDVGSGITVDYEGFGIGAISSSKRTDAONTAAYTGNGDRAE 240
QY 241 TYTGGLKYDANNITYLAQYOTYNATRVGSLG--ANKQNEEVAQYQFDEGLRPSLAYLQ 300
Db 241 TYTGGLKYDANNITYLAQYOTYNATRVGSLG--ANKQNEEVAQYQFDEGLRPSLAYLQ 300
QY 301 SKGNLGRGYDEDEILKYVDVGAATYFNKNMSTYVDYKINLDDNCFTRDAGINTDNIYA 360
Db 301 SKGNLGRGYDEDEILKYVDVGAATYFNKNMSTYVDYKINLDDNCFTRDAGINTDNIYA 360
QY 361 LGLVYQF 367
Db 361 LGLVYQF 367

```

RESULT 3

US-09-041-889-28

Sequence 28, Application US/09041889

Patent No. 6033864

GENERAL INFORMATION:

APPLICANT: Braun, Jonathan

APPLICANT: Conavy, Ofer

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, using

TITLE OF INVENTION: Microbial UC PANCA antigens

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,889

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/837,058

FILING DATE: 11-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-PM 3006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 28:

US-09-041-889-28

SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-889-28

Query Match 55.2%; Score 1078.5; DB 3; Length 323;
Best Local Similarity 66.2%; Pred. No. 1.5e-85;
Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps 9;

QY 1 MKSVLALLPALAAGAAHAAYNNKDGKLDYKVDGLHFRSDKKVDGDOTYRLG 60
DB 1 MKSVLALLPALAAGAAHAAYNNKDGKLDYKVDGLHFRSDKKVDGDOTYRLG 60
QY 61 FKGEVOTDITGQWEYDIOGNSAE--NENNSWTRVAFGLKRDQVGSFDYGNRVVY 119
DB 61 FKGEVOTDITGQWEYDIOGNSAE--NENNSWTRVAFGLKRDQVGSFDYGNRVVY 119
QY 120 DVTSMVDLPEFGDIT--GSDNFMQGRNFGATYRNTDFGLVDGLNFAVOYOGKNGNPS 178
DB 121 DIEWTMTLPEFGDSTNADNEMTGRANGVATYRNTDFGLVGLNFAVOYOGN---- 176
QY 179 GEGFTSGV--TNNGRDALRONGDVGSGITYDY--EGFGIGATSSSKRTDAQ--NTAAYI 233
DB 177 -EGASNGQECTNNGRDVREHNGDGMGLSTTYDLGMEFSAGAAYTSRDTNDQVNHAA-- 233
QY 234 GNGRATYTGKLYDANNITYLAQYTOTYNATRVSLGW--ANKAONFEVAVOYQDFG 291
DB 234 -GGKADAMTAGKLYDANNITYLATMYSETRNMPFGSDSDYAVANKTONFEVTAQYQDFG 292
QY 292 LRPSLAVLOSCKNL-----GRGYDDED 314
DB 293 LRPAVSFLMSKGRDLHAAGADNAGYVDKD 323

RESULT 4
US-08-355-844-1
; Sequence 1, Application US/08355844
; Patent No. 5940307
; GENERAL INFORMATION:
; APPLICANT: Fischbarg, Jorge
; APPLICANT: Czegledy, Ferenc
; APPLICANT: Iserovich, Pavel
; APPLICANT: Li, Jun
; APPLICANT: Cheung, Min
; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,844
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Tang, Henry Y.S.
; REGISTRATION NUMBER: 29,705
; REFERENCE/DOCKET NUMBER: A29927-50/29910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2586
; TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Escherichia coli
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..340
; OTHER INFORMATION: OmpF porin protein
US-08-355-844-1

Query Match 52.6%; Score 1027; DB 2; Length 340;
Best Local Similarity 58.4%; Pred. No. 4.5e-81;
Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

QY 22 AEVYKDGKLDLYKVDGLHFRS-----DNKVDGDOTYRLGFKGETOVDITGQY 76
DB 1 AEIYNKDGKVDLYKAVGLHYRSKGENSYGSGNDMTARLGFKGETQINSIDLITGQY 60
QY 77 WEYDIOGNSAEN--ENNSWTRVAFGLKRDQVGSFDYGRNVGVYDVTSMVDLPEFG 133
DB 61 WEYDIOGNSAEN--ENNSWTRVAFGLKRDQVGSFDYGRNVGVYDVTSMVDLPEFG 120
QY 134 DVTSGDNFMQGRNFGATYRNTDFGLVDGLNFAVOYOGKNGNSGSGFTSGVYNNGRD- 192
DB 121 DTAISDFEFGRVGCVATYRNSNFFGLVDGLNFAVOYLGK-----NBRDT 165
QY 193 ALRONGDVGSGITYDYEGFGIGATSSSKRTDAQONTAAVYINGDRAFETGGLKYDAN 252
DB 166 ARSNGDVGSGISYEBGFIYAGYADRTNQLD--AQPLGNKKAKDQATGLKYDAN 224
QY 253 IYLAQYTOTYNATRV-----GSLGMANKAONFEVAVOYQDFGLRSLAYLOSCKNGL 307
DB 225 IYLAANGETRNATPINKFTNTSGFANKTQDVLVAOYQDFGLRSLAYATKSKARDV- 283
QY 308 RGYDDEDILKVDYGAITYRNKNSTYVDYKINLLD--DNOFTRAGINTDITVALGLVQ 366
DB 284 EGIGDVLVWFEGVATYRNKNSTYVDYIINDISDNKL---GVGSDTVAVGVYQ 339
QY 367 F 367
DB 340 F 340

RESULT 5
PCT-US95-16126-1
; Sequence 1, Application PC/TUS9516126
; GENERAL INFORMATION:
; APPLICANT: Fischbarg, Jorge
; APPLICANT: Czegledy, Ferenc
; APPLICANT: Iserovich, Pavel
; APPLICANT: Li, Jun
; APPLICANT: Cheung, Min
; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25

```

:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/16126
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/355,844
: FILING DATE: 14-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Tang, Henry Y.S.
: REGISTRATION NUMBER: 29,705
: REFERENCE/DOCKET NUMBER: A29927-50/29910
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-408-2586
: TELEFAX: 212-765-2519
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 340 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Escherichia coli
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..340
: OTHER INFORMATION: OmpF porin protein
PCT-US95-16126-1
```

```

Query Match 52.6%; Score 1027; DB 5; Length 340;
Best Local Similarity 58.4%; Pred. No. 4.5e-81;
Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

QY 22 AEVYKDKNDLIDYKXVDLHYFS-----DNKVDSDQTYMRIGFKEGTQVTDQLTGYGQ 76
D6 1 AEITNKGKNDVLDYKAVGLHTRSKGENSYGSGNDMTARLQFKEGTQVTDQLTGIGQ 60
QY 77 WEYOIOGNSAEN---ENNSMTVAFAKLFQDVGSPDYGRNYGVYVYVSTVDVLPFEGG 133
D6 61 WEYFQGNNSGADAGQTKNTRLAFLAKYADVGSPDYGRNYGVYVYVSTVDVLPFEGG 120
QY 134 DTYSQDNFMQORNGFGATTYRTDFEGLVDGLNFAVYQKNGNPSGEGFTSGVTNNGRD- 192
D6 121 DTASDDEPFYGRGVGAVATYRNSNFEGLVDGLNFAVYQKNGNPSGEGFTSGVTNNGRD- 165
QY 193 ALRONGGVGSGITYDEGIGGAISSSKRTDAONTAAVYIGNDRABETVYGLKYDANN 252
D6 166 ARKNSGSGVSGISYEBGFEIGVAYGADRTNLOE--RQPLGNCKKADQWATGLKYDANN 224
QY 253 IYLAQYTQTYNATRV-----GSLGMANKAQNFEAVAQYQDFEGLRPSLAYLQSGKGNLG 307
D6 225 IYLAANGERRNATPIINKFTNTSGFANKQDVLVAQYQDFEGLRPSLAYLQSGKGNLG 283
QY 308 RGYDDEDLKTYDVGATYFENKKNSTYVDKINLLD--DNOFTRDAGINTDITVALGLVYQ 366
D6 284 EGIQDVLVNVFEVGATYFENKKNSTYVDYIINOISDKNL---GVGSDPTVAVGVYVQ 339
QY 367 F 367
D6 340 F 340
```

```

RESULT 6
US-08-096-181A-8
: Sequence 8, Application US/08096181A
: Patent No. 6153406
: GENERAL INFORMATION:
: APPLICANT: Tai, Joseph Y.
: APPLICANT: Pullen, Jeffrey K.
: APPLICANT: Soper, Thomas S.
: APPLICANT: Liang, Shu-Mei
: TITLE OF INVENTION: A Method For The High Level Expression,
```

```

:
: TITLE OF INVENTION: Purification And Refolding Of The Outer Membrane Protein
: TITLE OF INVENTION: P2 From Haemophilus Influenzae Type b
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/096,181A
: FILING DATE: 23-Jul-1993
: CLASSIFICATION: 424
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-096-181A-8
```

```

Query Match 8.4%; Score 164.5; DB 4; Length 361;
Best Local Similarity 24.1%; Pred. No. 1.4e-06;
Matches 90; Conservative 52; Mismatches 145; Indels 87; Gaps 17;

QY 4 KYALALLIPALLAGAAHAAEYNNKDKNLDYKVDGLHFSQDKVDGQGT-----56
D6 3 KTLAALIVGAFPAASANAAYNNNEGTVNELGGLSTIAEOS--NSTVDNQQOQHALRQ 61.
QY 57 -MRIGFGETQVTDQLTGCGYQWEXQIOGNSAENNSM---TRVAFGLKFDQVGSFDY 111
D6 62 GSRPHIKATINFGDGFYAGQYLETFRYTKASSENSDQFSGITSAVYVLTGNNAFGVKL 121
QY 112 GRNRYVYVYVTSWTDVLPFEGGDTYSGDNFMQORGN--FGATYRNTDFEGLVDGLNFAVYQ 170
D6 122 GRAFTIADGITSABD--KEYG--VLNNSDYIPTSNTVGYTFKQID--GLVLGANY---- 171
QY 171 QGRKNGNSGEGFTSGVTNNGRDALRONGDVGSGITYDEGIGGAISSSKRTDAONTA 230
D6 172 -----LLAQKREGAKG-----ENKRPNDKAGE 193
QY 231 AYIG---NGDRAETVTGLKYDANNIYLAQYTOT---YNATRVGSLGMANKAO--NFEA 282
D6 194 VRIGELNNGIQV-----GAKYDANDIYAKIATGNTNKYHESD-----EHKQOLNVL 242
QY 283 VAQYQF--DEGLRPSLAYLQSGKNGRGYDDEDLKTYDVGATYFENKKNSTYVDYKI-- 339
D6 243 TLGTYRFSDLGLVSLDGSYAKTKNYKIKHEKR--YVSPGFQYELMEDTNYVGNFKEYR 299
QY 340 NLDDNOFTRDAGI 353
D6 300 TSVDOGEKTRDQAV 313
```

```

RESULT 7
PCT-US94-08326-8
: Sequence 8, Application PC/TUS9408326
: GENERAL INFORMATION:
: APPLICANT: North American Vaccine, Inc.
: APPLICANT: 12103 Indian Creek Court
: APPLICANT: Beltsville, MD 20705
: APPLICANT: Pullen, Jeffrey K.
: APPLICANT: Soper, Thomas S.
```


1 APPLICANT: Liang, Shu-Mei
 2 TITLE OF INVENTION: A Method For The High Level
 3 TITLE OF INVENTION: Expression,
 4 TITLE OF INVENTION: Purification And Refolding Of The Outer Membrane
 5 TITLE OF INVENTION: Protein
 6 TITLE OF INVENTION: p2 From Haemophilus Influenzae Type b
 7 NUMBER OF SEQUENCES: 14
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 10 STREET: 1100 New York Avenue, Suite 600
 11 CITY: Washington
 12 STATE: D.C.
 13 COUNTRY: U.S.A.
 14 ZIP: 20005-3934
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Patent In Release #1.0, Version #1.25
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: PCT/US94/08326
 22 FILING DATE: Herewith
 23 CLASSIFICATION:
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: US 08/096,181
 26 FILING DATE: 23-JULY-1993
 27 ATTORNEY/AGENT INFORMATION:
 28 NAME: Esmond, Robert W.
 29 REFERENCE/DOCKET NUMBER: 1438.001PC01
 30 TELECOMMUNICATION INFORMATION:
 31 TELEPHONE: (202) 371-2600
 32 TELEFAX: (202) 371-2540
 33 INFORMATION FOR SEQ ID NO: 8:
 34 SEQUENCE CHARACTERISTICS:
 35 LENGTH: 361 amino acids
 36 TYPE: amino acid
 37 TOPOLOGY: linear
 38 MOLECULE TYPE: protein
 39 PCT-US94-08326-8

	Query Match	8.4%:	Score 164.5:	DB 5:	Length 361:	
	Best Local Similarity	24.1%:	Pred. NO.1.4e-06:			
	Matches	90:	Conservative	52:	Mismatches 145:	Indels 87: Gaps 17.
OY	4	KVLLALLIPALLAAGAAHAAEVYNKDGKNLTDLYGKVDGLHFEFNDKRDVDDQTY-----	56			
Db	3	KTIALIYGAFASANAANAVYYNNNGTSINVELCGRLSIIAEGS--NSTVDNQKQHGAIRMQ	61			
OY	57	-MRLGFKETOVITDOLITGYGOMEIVIQGSNAENENNSW----TRAFACIAKFDYDVSFDY	111			
Db	62	GSRFIPIKTHNEGDGFYAQYLTEFRFTVASGENSGDNFGDIYSKAAYVLGNKARGEVKL	121			
OY	112	GRNYGVVVDTYSMTVDLPDFEFGDYTGSDNFMQRQSN--FCATYRNTDFGLVGLNPAVOY	170			
Db	122	GRAKTIAGIITSABD--KEYG--VLNNSDYIPTSGNTYGTPTKGID--GLVIGANY----	171			
OY	171	OGKNCNPSEGEFTSCVTNNRGDALPQNDGCVGGSTFYDIEGFIGCAISSSKRTDAQNTA	230			
Db	172	-----LLAQKREGAAG-----	193			
OY	231	AYIG--NGDRAETYTGKLTADANNIYLAOCTOF---YNATRVSGLGWANKAO--NFEA	282			
Db	194	VRIGINNGIOY-----GAKTDANDIVAKIAGRPNRYKTNESD-----EHKQQLNGVLA	242			
OY	283	VAOYQV--DFGLRPISLAYLOSKGKNLRGCVDEDDILKYVDVGATYYYFNKNMSTYVDYKI--	339			
Db	243	TLYGFFSLDLGLSVLSDSGCAKTKNKYIKIHKKR---YFSPSGOYEIMEDTNYGCMFKYER	299			
OY	340	NLLDDNQTFRADGI	353			
Db	300	TSSVDGCKTRDOAV	313			

RESULT 8
 US-08-096-182A-4
 Sequence 4, Application US/08096182A
 Patent No. 5439608
 GENERAL INFORMATION:
 APPLICANT: Blake, Milan S.
 APPLICANT: Tai, Joseph Y.
 APPLICANT: Qi, Huijin L.
 APPLICANT: Liang, Shu-Mei
 APPLICANT: Hronowski, Lucjan J.J.
 APPLICANT: Pullen, Jeffrey K.
 TITLE OF INVENTION: Method for the High Level Expression,
 TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Protein B
 TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/096,182A
 FILING DATE: 23-JUL-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 1438, 0060000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-096-182A-4

[illegible]

Db 132 EISVRD-----SPVFAGSGSVQYVPRDNANDYKRYKHTKSSRSRYHAGLKYENAGFFGQ 187
QY 216 GAISSSK-----RTDAONTAAYIGNGDRAETY-----TGGLKYDANNY--LAAQYTOTN 264
Db 188 YAGSFAYADLNTDAEVAANTANAHFVKDYQYHRYVAG--TDANDLYVYAGQYEAKN 245
QY 265 ATRVGS-GMANKAONEEAVAYOYQDFGLRPSLAYLOS-KGNLKG--RGYDDEDILKYV 319
Db 246 -NEVGSFKGKHQOTYAATAAYRFG-NVTPRVSYAHGFAYKNGVGDANDYQYDOYI--- 300
QY 320 DVGATYFENKMSITYV 335
Db 301 -VGADYDFSKRTSALV 315

RESULT 11
PCT-US94-08327-4

Sequence 4, Application PC/TUS9408327
GENERAL INFORMATION:
APPLICANT: The Rockefeller University
APPLICANT: 1230 York Avenue
APPLICANT: New York, New York 10021
APPLICANT: United States of America
APPLICANT: 12103 Indian Creek Court
APPLICANT: Beltsville, Maryland 20705
APPLICANT: United States of America
APPLICANT: Tai, Joseph Y.
APPLICANT: Qi, Hulin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Hironowski, Lucjan J.J.
TITLE OF INVENTION: Method for the High Level
TITLE OF INVENTION: Expression,
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane
TITLE OF INVENTION: Group B
NUMBER OF INVENTION: Porin Proteins from Neisseria Meningitidis
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08327
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,182
FILING DATE: 23 July 1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.006PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-08327-4

Query Match

7.2%; Score 140.5; DB 5; Length 342;

Best Local Similarity 25.6%; Pred. No. 0.00015;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLFKFGQYTDLTGQWQYQIQGSAENENNSW-TRAFAGLKRFQDVGSPDYGR--N 114
Db 43 KIFKQGEIDLGNGKAIWOLE--QKASIAQTNSGNGNSPFLGLK---GGFGYVAGN 95
QY 115 YGVVY-----DVSMIDVLEDFPGDGYGSDNFMQQRNGFATYRNTDFGL-----VDGL 164
Db 96 LNTVLDGSDGNVANM-----ESGSNT-----EVLGLGTIGRVER 131
QY 165 NFAVYQGNKNGPSGEGFTSGV-----TNNGRDA-----LNQNDGVGGSITTYDEGCGIG 215
Db 132 EISVRD-----SPVFAGSGSVQYVPRDNANDYKRYKHTKSSRSRYHAGLKYENAGFFGQ 187
QY 216 GAISSSK-----RTDAONTAAYIGNGDRAETY-----TGGLKYDANNY--LAAQYTOTN 264
Db 188 YAGSFAYADLNTDAEVAANTANAHFVKDYQYHRYVAG--TDANDLYVYAGQYEAKN 245
QY 265 ATRVGS-GMANKAONEEAVAYOYQDFGLRPSLAYLOS-KGNLKG--RGYDDEDILKYV 319
Db 246 -NEVGSFKGKHQOTYAATAAYRFG-NVTPRVSYAHGFAYKNGVGDANDYQYDOYI--- 300
QY 320 DVGATYFENKMSITYV 335
Db 301 -VGADYDFSKRTSALV 315

RESULT 12

US-08-096-182A-6
Sequence 6, Application US/08096182A
Patent No. 5439808
GENERAL INFORMATION:
APPLICANT: Blake, Milan S.
APPLICANT: Tai, Joseph Y.
APPLICANT: Qi, Hulin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Hironowski, Lucjan J.J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the High Level Expression,
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,182A
FILING DATE: 23-JUL-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0060000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-182A-6


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REFERENCE/DOCKET NUMBER: 1438.0060002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-760-6

Query Match
Best Local Similarity 7.2%; Score 140.5; DB 3; Length 363;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLGFKEGTQYTDLTGYGWEYQIQNSAENENNSW-TRVAFAGLKFQDVSFDYGR--N 114
:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 KIGFKGEDLGNCKMKAIMOLE---QKASIAGTNSGWNRSQSFGLK---GFGTVRAGN 116
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 YGVVY-----DVTSMIDVLEPFGDPTYGSDNFMQQRNPFATYRNDPFGT-----VDGL 164
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117 LNTVLKDSGDNVNMW-----ESSNT-----EDVLGLGTIGRVER 152
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 165 NFAVOYQKNGNPSGEGFTSGV-----TNGRDA-----LRONGDVGGSITYDEGFGIG 215
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 153 EISVRVD---SPVFAFGSSGYQVPRDNANDVDKYKHTKSSRSYHAGLKYENAGFGQ 208
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 216 GAISSSK---RTDAONTAAYIGNGDRAEY-----TGILKYDANNY--LAAQYTOTYN 264
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 209 YACSFAYADLNTDAERVAANTANAHFVKDYHVRVAG--YDANDLYVSAGQYEAAKN 266
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 265 ATRVGSU-GWANKAQNENVAOYQFDGLRPSLAYLOS-KGKNG---RGYDDEDILKYV 319
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 -NEVSGTKGKKHETQYAAATPAATPFG-NVTPRVSYAHGFAKAVNGVDANTYTDQYI--- 321
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 320 DVGATYYFNKNMSTYV 335
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 322 -VGADYDFSKRTSATLV 336
: : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 15
PCT-US94-08327-6
Sequence 6, Application PC/TUS9408327
GENERAL INFORMATION:
APPLICANT: The Rockefeller University
APPLICANT: 1230 York Avenue
APPLICANT: New York, New York 10021
APPLICANT: United States of America
APPLICANT: 12103 Indian Creek Court
APPLICANT: Beltsville, Maryland 20705
APPLICANT: United States of America
APPLICANT: Tai, Joseph Y.
APPLICANT: Qi, Hulin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Hironowski, Lucjan J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the High Level
TITLE OF INVENTION: Expression,
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane
TITLE OF INVENTION: Group B
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08327
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,182
FILING DATE: 23 July 1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 1438.006PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-08327-6

Query Match
Best Local Similarity 7.2%; Score 140.5; DB 5; Length 363;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLGFKEGTQYTDLTGYGWEYQIQNSAENENNSW-TRVAFAGLKFQDVSFDYGR--N 114
:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 KIGFKGEDLGNCKMKAIMOLE---QKASIAGTNSGWNRSQSFGLK---GFGTVRAGN 116
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 YGVVY-----DVTSMIDVLEPFGDPTYGSDNFMQQRNPFATYRNDPFGT-----VDGL 164
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117 LNTVLKDSGDNVNMW-----ESSNT-----EDVLGLGTIGRVER 152
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 165 NFAVOYQKNGNPSGEGFTSGV-----TNGRDA-----LRONGDVGGSITYDEGFGIG 215
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 153 EISVRVD---SPVFAFGSSGYQVPRDNANDVDKYKHTKSSRSYHAGLKYENAGFGQ 208
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 216 GAISSSK---RTDAONTAAYIGNGDRAEY-----TGILKYDANNY--LAAQYTOTYN 264
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 209 YACSFAYADLNTDAERVAANTANAHFVKDYHVRVAG--YDANDLYVSAGQYEAAKN 266
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 265 ATRVGSU-GWANKAQNENVAOYQFDGLRPSLAYLOS-KGKNG---RGYDDEDILKYV 319
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 -NEVSGTKGKKHETQYAAATPAATPFG-NVTPRVSYAHGFAKAVNGVDANTYTDQYI--- 321
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 320 DVGATYYFNKNMSTYV 335
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 322 -VGADYDFSKRTSATLV 336
: : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: September 25, 2001, 15:54:31
Job time: 70 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 ; Search time 16.07 Seconds

(without alignments)
1739.643 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953
Sequence: 1 MKSKVLLALIPALLAAGAAH.....TRDAGINTDNIVALGLVYQF 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	1 MMECPC	outer membrane por
2	1804	92.4	367	2 B85861	outer membrane por
3	1539.5	78.8	378	1 MMEBPC	outer membrane por
4	1537	78.7	363	2 S51104	outer membrane por
5	1512.5	77.4	378	1 A59139	outer membrane por
6	1295	66.3	377	2 D64888	outer membrane por
7	1213.5	62.1	394	2 S34263	outer membrane por
8	1177	60.3	365	1 MMECNC	outer membrane por
9	1174	60.1	365	1 MMEBPC	outer membrane por
10	1142.5	58.5	366	2 E85729	probable outer mem
11	1109	56.8	351	1 MMECPE	outer membrane por
12	1109	56.8	351	2 B85513	outer membrane por
13	1104	56.5	362	1 MMECF	outer membrane por
14	1104	56.5	362	2 B85619	outer membrane por
15	1086	55.6	351	2 S25520	outer membrane por
16	1065.5	54.6	350	2 S25525	outer membrane por
17	1055.5	54.0	350	2 S36806	outer membrane por
18	1027.5	52.6	363	2 S43159	outer membrane por
19	1002	51.3	369	2 S70847	outer membrane por
20	733.5	37.6	255	2 D85740	partial probable o
21	732	37.5	315	2 T46993	hypothetical prote
22	692	35.4	224	2 F85814	probable outer mem
23	600	30.7	171	2 H64960	outer membrane por
24	592	30.3	382	2 G84971	ompF-like porin [I
25	522.5	26.8	123	2 C85740	partial probable o
26	478	24.5	191	2 G85814	probable outer mem
27	388.5	19.9	134	2 B64961	outer membrane por
28	310	15.9	96	2 C64900	outer membrane por
29	279	14.3	350	2 A82299	outer membrane pro

30	254	13.0	331	2 E82389	probable outer mem
31	215.5	11.0	97	2 A57983	outer membrane por
32	194.5	10.0	371	2 S68072	major outer membra
33	194.5	10.0	371	2 S68069	major outer membra
34	176	9.0	386	2 S68062	major outer membra
35	174.5	8.9	326	2 JN0792	porin-like protein
36	173.5	8.9	385	2 S68066	major outer membra
37	172.5	8.8	385	2 S68067	major outer membra
38	169.5	8.7	385	2 S68070	major outer membra
39	169	8.7	50	2 T46990	hypothetical prote
40	168.5	8.6	361	2 JC6314	major porin protei
41	165	8.4	330	2 PC4425	lectin-like adhesi
42	164.5	8.4	361	2 A30542	major outer membra
43	163.5	8.4	359	2 D64050	major outer membra
44	156.5	8.0	368	2 A82148	probable porin VC1
45	155	7.9	360	2 S17456	outer membrane pro

ALIGNMENTS

RESULT 1
MMECPC
outer membrane porin ompC precursor - Escherichia coli
C/Spectes: Escherichia coli
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C/Accession: A20867; A18885; B25029; E64991
R/Mizuno, T.; Chou, M.Y.; Inouye, M.
J. Biol. Chem. 258, 6932-6940, 1983
A/Title: A comparative study on the genes for three porins of the Escherichia coli ou
A/Reference number: A20867; MUID:83213433
A/Accession: A20867
A:Molecule type: DNA
A:Residues: 1-367 <MIZ>
A:Cross-references: GB:K00541; GB:M10314; GB:M14188; NID:q147007; PIDN:AAA24243.1; PI
R/Mizuno, T.; Chou, M.Y.; Inouye, M.
FEBS Lett. 151, 159-164, 1983
A/Title: DNA sequence of the promoter region of the ompC gene and the amino acid sequ
A/Reference number: A18885; MUID:83132326
A/Accession: A18885
A:Molecule type: DNA
A:Residues: 1-40 <MIZ>
R/Nogami, T.; Mizuno, T.; Mizushima, S.
J. Bacteriol. 164, 797-801, 1985
A/Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous r
A/Reference number: A91809; MUID:86033642
A/Accession: B25029
A:Molecule type: DNA
A:Residues: 32-57 <NOG>
A:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617
A/Accession: E64991
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-367 <BLAT>
A:Cross-references: GB:AE000310; GB:U00096; NID:q2367131; PIDN:AACT5275.1; PID:q17885
C/Genetics:
A:Gene: ompC
A:Map position: 47 min
C/Function:
A:Description: one of the E. coli major outer membrane proteins that form passive dif
C:Superfamily: outer membrane protein porin
C:Keywords: membrane protein; porin; trimer
F:1-21/Domain: signal sequence #status predicted <Sig>
F:22-367/Product: outer membrane porin ompC #status predicted <Mat>

Query Match 98.0%; Score 1914; DB 1; Length 367;
Best Local Similarity 98.1%; Pred. No. 5.6e-127;

Query Match 60.1%; Score 1174; DB 1; Length 365;
Best Local Similarity 62.1%; Pred. No. 4e-75;
Matches 234; Conservative 41; Mismatches 80; Indels 22; Gaps 6;

Query 1 MRSKVLAL--LIPALLAAGAAHAEVYNNKDKGKLDLYGKVDGLHFSFNDKDVDDQTYMR 58
Db 1 MKRTIYVAVVAASVLMAMSAQAHEITNKSNDKLDLYGKVAHAKHYSSNDADGDTTYAR 60
QY 59 LGFGEQTQVTDLTGYGQWEYQIOGNSAENENNS--WTRVAFAGLKFQDVGSEPDYGRNYG 116
Db 61 LGFGEQTQVTDLTGYGQWEYQIOGNSAENENNS--WTRVAFAGLKFQDVGSEPDYGRNYG 120
QY 117 VVVDYTSWTDVLPFEGGDTY--GSDNFMQORGNFATYRNTDFGLVDGLNFAVOYQKNG 175
Db 121 VVVDYTSWTDVLPFEGGDTY--GSDNFMQORGNFATYRNTDFGLVDGLNFAVOYQKNG 180
QY 117 VVVDYTSWTDVLPFEGGDTY--GSDNFMQORGNFATYRNTDFGLVDGLNFAVOYQKNG 175
Db 121 VVVDYTSWTDVLPFEGGDTY--GSDNFMQORGNFATYRNTDFGLVDGLNFAVOYQKNG 180
QY 176 NPSGEFTSGVTNNGRDALRQNGDVGGSITDYEGFGIGALSSSKRTDAQNTAAV-- 233
Db 181 RSPFDNTBEG-----NGDGFESATYEEGFGICATATYAKSDRTDTQVNAKGLVP 229
QY 234 ---GNQDRAETTYGGLKYDANNITYLAAQYTYTNATRVGSLGMANKAQNFEAAVQYQDF 290
Db 230 EVFASGKNAEVAAGLKYDANNITYLATYSETQMTVFADHPVANKAQNFEAAVQYQDF 289
QY 291 GLRPSLAYIOSKGNLGRGVDDDLKYVDVGATYFNKMSYVVDYKINLIDNOQTRD 350
Db 290 GLRPSVAYIOSKGRDLG--VWGDDDLKYVDVGATYFFKNMSTFVDYKINLIDKNDETKA 348
QY 351 AGINTDNIVALGLVYQF 367
Db 349 LGVSTDDIVAVGLVYQF 365

RESULT 9
MMBP2
outer membrane porin lc precursor - phage PA2
C:Species: phage PA2
A:Note: host Escherichia coli
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 02-Jul-1998
C:Accession: D25647
R:Blasband, A.J.; Marcotte Jr., W.R.; Schnaitman, C.A.
J. Biol. Chem. 261, 12723-12732, 1986
A:Title: Structure of the lc and nmpc outer membrane porin protein genes of lambdaoid bac
A:Reference number: A25647; MVID:86304457
A:Accession: D25647
A:Molecule type: DNA
A:Residues: 1-365 <BLA>
C:Genetics:
A:Gene: lc
C:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimmer
F:1-23/Domain1: signal sequence #status predicted <Sig>
F:24-365/Product: outer membrane porin lc #status predicted <Mat>

Query Match 58.5%; Score 1142.5; DB 2; Length 366;
Best Local Similarity 59.9%; Pred. No. 6.3e-73;
Matches 226; Conservative 45; Mismatches 85; Indels 21; Gaps 6;

Query 1 MRSKVLALLIPALLAAGAAHAEVYNNKDKGKLDLYGKVDGLHFSFNDKDVDDQTYMR 60
Db 1 MKRTIYVAVVYTGILLANVAHAEVYNNKDKGKLDLYGKVAHAKHYSSNDADGDTTYAR 60
QY 61 FKGEQTQVTDLTGYGQWEYQIOG--NSAENENNSWTRVAFAGLKFQDVGSEPDYGRNYG 118
Db 61 FKGEQTQVTDLTGYGQWEYQIOG--NSAENENNSWTRVAFAGLKFQDVGSEPDYGRNYG 120
QY 119 YDTSWTDVLPFEGGDTY--GSDNFMQORGNFATYRNTDFGLVDGLNFAVOYQKNG 177
Db 121 YDTSWTDVLPFEGGDTY--GSDNFMQORGNFATYRNTDFGLVDGLNFAVOYQKNG 179
QY 178 SGEFTSGVTNN---GRDALRQNGDVGGSITDYEGFGIGALSSSKRTDAQNTAA-- 231
Db 180 -----TDNSHLTYGADYTRANGDFGSISSITYVDGFGIGAVYTSKRTDAQNTAA-- 230
QY 232 -YICNGDRAETTYGGLKYDANNITYLAAQYTYTNATRVGSLGMANKAQNFEAAVQYQDF 290
Db 231 PLNASKNAELMAGIKYDANNITYFAANVETLMTYTGDIYSKNAQSEVVAQYQDF 290
QY 291 GLRPSLAYIOSKGNLGRGVDDDLKYVDVGATYFNKMSYVVDYKINLIDNOQTRD 350
Db 291 GLRPSLAYIOSKGNLGRGVDDDLKYVDVGATYFNKMSYVVDYKINLIDNOQTRD 349
QY 351 AGINTDNIVALGLVYQF 367
Db 350 VDIRTDIVAVGITYQF 366

RESULT 11
MMECP2
outer membrane porin phoE precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A03432; B64749
J. Mol. Biol. 163, 513-532, 1983
A:Title: Complete nucleotide sequence of phoE, the structural gene for the phosphate
A:Reference number: A92893; MVID:83189086
A:Accession: A03432

A.Molecule type: protein
 A.Residues: 23-87, 'E', 89-138, 'G', 140-283, 'L', 285-362 <CHE>
 R.Nogami, T.; Mizuno, T.; Mizushima, S.
 J. Bacteriol. 164, 797-801, 1985
 A.Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous recombination
 A.Reference number: A91809; MUID:86033642
 A.Accession: A25029
 A.Molecule type: DNA
 A.Residues: 33-63 <NOC>
 R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A.Title: The complete genome sequence of *Escherichia coli* K-12.
 A.Reference number: A64720; MUID:97426617
 A.Accession: H64832
 A.Status: nucleic acid sequence not shown; translation not shown
 A.Molecule type: DNA
 A.Residues: 1-362 <BLAT>
 A.Cross-references: GB:AE000195; GB:U00096; NID:91787156; PIDN:AMC74015.1; PID:91787160;
 A.Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: ompF; tolF; cmfB; coa; cry
 A:Map position: 21 min
 C:Complex: homotrimer
 C:Function: <POK>
 A:Description: Forms aqueous channels that facilitate diffusion of small hydrophilic mole
 C:Function: <REC>
 A:Description: receptor for bacteriophage T2
 C:Superfamily: outer membrane protein phoE
 C:Keywords: membrane protein; porin; trimer
 F:1-22/Domain: signal sequence #status predicted <STG>
 F:23-362/Product: outer membrane porin ompF #status experimental <MAT>

Query Match 56.5%; Score 1104; DB 1; Length 362;
 Best Local Similarity 58.9%; Pred. No. 3.2e-70;
 Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;

1 MKSKVLALLIPALLAAGAAAEVYKNDGNKLDLYGKVDGLHYFS-----DNKVDGDOT 55
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 2 MKRNILAVIPALLVAGTANAAEITKNDGNKVDLYGKAGLHFSKNGENSYGNGDMT 61
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 56 YARLGEKGETQVTDLTGYGWEYQIQNSAEN---ENNSWTRVAPAGLKFODVGSFDYG 112
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 62 YARLGEKGETQVTDLTGYGWEYQIQNSAEN---ENNSWTRVAPAGLKFODVGSFDYG 121
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 113 RNVGVYDVTSMVDLPREGSDPTGSDNFMQGRNGATYRMTDFGLVDGLNFAVQYIG 172
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 122 RNVGVYDVTSMVDLPREGSDPTGSDNFMQGRNGATYRMTDFGLVDGLNFAVQYIG 181
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 173 KNGNPSGEFTSGVTNNGRD-ALRONGDVGSGITVDYEGFGIGAISSSKRTDAQNTAA 231
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 182 K-----NENDTARNSMGDVGSGISYEYGFVAGYGAADRTNIDF-AQ 225
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 232 YVGNDRATYTGGLKYDANNITYLAAQYQTYNATRV-----GSLGAKAONFEAVAY 286
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 226 PLGNGKKAQOMATGKLYDANNITYLAAQYQTYNATRV-----GSLGAKAONFEAVAY 285
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 287 QPFDGRLPSLATYLSKGLRGYDDEDILKYVDGATYFKNMSTYVDYKINLLD-DN 345
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 286 QPFDGRLPSLATYLSKGLRGYDDEDILKYVDGATYFKNMSTYVDYKINLLD-DN 344
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 346 QPFDGRLPSLATYLSKGLRGYDDEDILKYVDGATYFKNMSTYVDYKINLLD-DN 345
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 345 KL----GVGSDPTVAVGIYQF 362

RESULT 14
 B85619
 outer membrane protein 1a (Ia,b,F) [imported] - *Escherichia coli* (strain O157:H7)
 C:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 C:Accession: B85619

R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Llim, A.; Diallanata, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A.Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A.Reference number: A65480; MUID:21074935; PMID:11206551
 A.Accession: B85619
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-362 <STO>
 A.Cross-references: GB:AE005174; NID:912514104; PIDN:AA655414.1; GSPDB:GN00145; UWGP:
 A.Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ompF
 C:Superfamily: outer membrane protein phoE

Query Match 56.5%; Score 1104; DB 2; Length 362;
 Best Local Similarity 58.9%; Pred. No. 3.2e-70;
 Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;

1 MKSKVLALLIPALLAAGAAAEVYKNDGNKLDLYGKVDGLHYFS-----DNKVDGDOT 55
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 2 MKRNILAVIPALLVAGTANAAEITKNDGNKVDLYGKAGLHFSKNGENSYGNGDMT 61
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 56 YARLGEKGETQVTDLTGYGWEYQIQNSAEN---ENNSWTRVAPAGLKFODVGSFDYG 112
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 62 YARLGEKGETQVTDLTGYGWEYQIQNSAEN---ENNSWTRVAPAGLKFODVGSFDYG 121
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 113 RNVGVYDVTSMVDLPREGSDPTGSDNFMQGRNGATYRMTDFGLVDGLNFAVQYIG 172
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 122 RNVGVYDVTSMVDLPREGSDPTGSDNFMQGRNGATYRMTDFGLVDGLNFAVQYIG 181
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 173 KNGNPSGEFTSGVTNNGRD-ALRONGDVGSGITVDYEGFGIGAISSSKRTDAQNTAA 231
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 182 K-----NENDTARNSMGDVGSGISYEYGFVAGYGAADRTNIDF-AQ 225
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 232 YVGNDRATYTGGLKYDANNITYLAAQYQTYNATRV-----GSLGAKAONFEAVAY 286
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 226 PLGNGKKAQOMATGKLYDANNITYLAAQYQTYNATRV-----GSLGAKAONFEAVAY 285
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 287 QPFDGRLPSLATYLSKGLRGYDDEDILKYVDGATYFKNMSTYVDYKINLLD-DN 345
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 286 QPFDGRLPSLATYLSKGLRGYDDEDILKYVDGATYFKNMSTYVDYKINLLD-DN 344
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 346 QPFDGRLPSLATYLSKGLRGYDDEDILKYVDGATYFKNMSTYVDYKINLLD-DN 345
 || :|||:||||| || :|||:|||||:||||| ||||| :||| :|||
 345 KL----GVGSDPTVAVGIYQF 362

RESULT 15
 S25520
 outer membrane porin phoE precursor - *Citrobacter freundii*
 C:Species: *Citrobacter freundii*
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
 C:Accession: S25520
 R.Spiersing, G.; Ockhuysen, C.; Hofstra, H.; Tommassen, J.
 submitted to the EMBL Data Library, August 1992
 A.Reference number: S25520
 A.Accession: S25520
 A.Molecule type: DNA
 A.Residues: 1-351 <SP1>
 A.Cross-references: EMBL:X68021; NID:940474; PIDN:CAA48162.1; PID:940475
 A.Note: this is one of the proteins induced when the *E. coli* cells are grown under ph
 d compounds, and some other negatively charged solutes
 C:Genetics:
 A:Gene: phoE
 C:Complex: homotrimer
 C:Function:
 A:Description: allows passive diffusion of small hydrophilic molecules with molecular
 A:Note: induced under phosphate limitation
 C:Superfamily: outer membrane protein phoE
 C:Keywords: homotrimer; membrane protein; porin
 F:1-21/Domain: signal sequence #status predicted <STG>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 ; Search time 13.11 Seconds

(without alignments)
958.945 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953

Sequence: 1 MKSKVALLIPALLAGAAH.....TRDAGITFDNIVALGLVYQF 367

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	1	OMP_C_ECOLI
2	1539.5	78.8	378	1	OMP_C_SALTI
3	1537	78.7	363	1	OMP_C_KLEPN
4	1512.5	77.4	378	1	OMP_C_SALTY
5	1296	66.4	383	1	OMP2_SALTI
6	1295	66.3	377	1	OMP_N_ECOLI
7	1283.5	65.7	376	1	OMP_C_SERNA
8	1241	63.5	374	1	OMP_C_SERNA
9	1220	62.5	342	1	OMP_C_RAHMO
10	1213.5	62.1	394	1	OMSI_SALTI
11	1187	60.8	397	1	YEDS_ECOLI
12	1177	60.3	365	1	NMPC_ECOLI
13	1169	59.9	365	1	PORI_BPPA2
14	1129.5	57.8	350	1	PHOE_ENTCI
15	1109	56.8	351	1	PHOE_ECOLI
16	1104	56.5	362	1	OMP_F_ECOLI
17	1086	55.6	351	1	PHOE_CITFR
18	1065.5	54.6	350	1	PHOE_SALTY
19	1060	54.3	349	1	PHOE_KLEPX
20	1059	54.2	351	1	PHOE_KLEPX
21	1055.5	54.0	350	1	PHOE_SALTI
22	1029.5	52.7	363	1	OMP_F_SALTI
23	1027.5	52.6	363	1	OMP_F_SALTY
24	1002	51.3	369	1	OMP_F_XENNE
25	882	45.2	282	1	OMP_C_SALTY
26	592	30.3	382	1	PORL_BUCAI
27	289	14.8	341	1	OMP_L_PHORP
28	279	14.3	341	1	OMP_U_VIBCH
29	196	10.0	363	1	OM2B_HAEIN
30	194.5	10.0	367	1	OM2A_HAEIN
31	194.5	10.0	371	1	OM25_HAEIN
32	192.5	9.9	361	1	OM29_HAEIN
33	191.5	9.8	369	1	OM27_HAEIN

34	189	9.7	360	1	OM26_HAEIN	O48216 haemophilus
35	187.5	9.6	353	1	OM28_HAEIN	O48221 haemophilus
36	176	9.0	386	1	OM24_HAEIN	P46026 haemophilus
37	174.5	8.9	326	1	OMPH_PHORP	P29739 photobacter
38	173.5	8.9	385	1	OM23_HAEIN	P46025 haemophilus
39	164.5	8.4	361	1	OM22_HAEIN	P20149 haemophilus
40	163.5	8.4	359	1	OM21_HAEIN	P43839 haemophilus
41	154	7.9	348	1	OM22_NEIGO	P20148 neisseria g
42	153	7.8	348	1	OM21_NEIGO	P18195 neisseria g
43	152.5	7.8	385	1	OMP_BORPE	O04064 bordetella
44	141	7.2	351	1	OM32_COMAC	P24305 comamonas a
45	140	7.2	393	1	OM21_NEIMC	P13415 neisseria m

ALIGNMENTS

RESULT 1 :
OMP_C_ECOLI
ID OMP_C_ECOLI STANDARD: PRT; 367 AA.
AC P06996;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMP_C) (OUTER MEMBRANE
PROTEIN 1b).
GN OMP_C OR MEOA OR PAR.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP MEDLINE=83213433; PubMed=6304064;
RX MEDLINE=83213433; PubMed=6304064;
RA Mizuno T., Chou M.-Y., Inouye M.;
RT coli outer membrane. DNA sequence of the osmoregulated ompc gene.;
RL J. Biol. Chem. 258:6932-6940(1983).
RN [2]
RP MEDLINE=97251358; PubMed=9097040;
RX MEDLINE=97251358; PubMed=9097040;
RC STRAIN=K12;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakabe S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampo K., Seki Y., Sivasubramanian S., Tagami H.,
RA Takada J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP MEDLINE=83132326; PubMed=6297988;
RX MEDLINE=83132326; PubMed=6297988;
RT "Mizuno T., Chou M.-Y., Inouye M.;
acid sequence of the signal peptide of pro-omp protein of

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RT Escherichia coli."
RN FEBS Lett. 151:159-164(1983).
RP SEQUENCE OF 32-57 FROM N.A.
RX MEDLINE=86033642; PubMed=2997131;
RA Nogami T., Mizuno T., Mizushima S.;
RT "Construction of a series of ompF-ompC chimeric genes by in vivo
RT homologous recombination in Escherichia coli and characterization of
RT the translational products."
RL J. Bacteriol. 164:797-801(1985).
RN [7]
RP SEQUENCE OF 22-30.
RX STRAIN-K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
RN [8]
RP SEQUENCE OF 22-26.
RX STRAIN-K12 / W3110;
MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT "Extraction of membrane proteins by differential solubilization for
RT separation using two-dimensional gel electrophoresis."
RL Electrophoresis 19:837-844(1998).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHO FAMILY OF PORINS.
CC -----
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CC -----
DR EMBL: K00541; AAA24243.1; -
DR EMBL: AE000310; AAC75275.1; -
DR EMBL: D90850; BAA15998.1; -
DR EMBL: U00008; AAA16412.1; -
DR PIR: A20867; MMECP.
DR PIR: B25029; B25029.
DR PIR: A18885; A18885.
DR HSP: P02931; IGFN.
DR ECO2DBASE; A035.5; 6TH EDITION.
DR EcoGene; E610670; ompC.
DR InterPro; IPR001702; -
DR InterPro; IPR001897; -
DR Pfam; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLI_PORIN.
DR PRINTS; PR00183; ECOLI_PORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Phage recognition; signal.
FT SIGNAL 1 21
FT CHAIN 1 367
FT SEQUENCE 367 AA; 40368 MW; 6AA9370CC8A1A225 CRC64;
SO

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Query Match 98.0%; Score 1914; DB 1; Length 367;
Best Local Similarity 98.1%; Pred. No. 7.8e-126;
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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OY 1 MSKVTALLIPALLAAGAAHAFAVYKDKGKLDYKVDGLAHFSPNKKVDGQDTYMRIG 60
DB 1 MKKVTLLVLPALVAGAAAEVYKDKGKLDYKVDGLAHFSPNKKVDGQDTYMRIG 60
OY 61 FKGEQVTDQLTGYGQWEXQIOGNSAENENNSWTRVAFAGLKPDYGVSGFYGVVD 120
DB 1 FKGEQVTDQLTGYGQWEXQIOGNSAENENNSWTRVAFAGLKPDYGVSGFYGVVD 120

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DB 61 FKGEQVTDQLTGYGQWEXQIOGNSAENENNSWTRVAFAGLKPDYGVSGFYGVVD 120
OY 121 VTSWTPVLPFGGDTYGSNFMQGRNFGATYRNTPFGLYVSLANFAVOYQGNKNGPSE 180
DB 121 VTSWTPVLPFGGDTYGSNFMQGRNFGATYRNTPFGLYVSLANFAVOYQGNKNGPSE 180
OY 181 GFTSGVTNNGRDALRONGDVGSGITYDEGFGIGAISSSKRTDQNTAAAYIGNGDRAE 240
DB 181 GFTSGVTNNGRDALRONGDVGSGITYDEGFGIGAISSSKRTDQNTAAAYIGNGDRAE 240
OY 241 TYTGGLKYDANNIYLAQTYQTYNATRVGSLGANKAQNFEAVAYQFDPGLRPSLAYIQ 300
DB 241 TYTGGLKYDANNIYLAQTYQTYNATRVGSLGANKAQNFEAVAYQFDPGLRPSLAYIQ 300
OY 301 SKKKNRGCGYDDDDILKYDVGATYFNKNMSTYVYKTNLDDNQFTDAGINTDNTYA 360
DB 301 SKKKNRGCGYDDDDILKYDVGATYFNKNMSTYVYKTNLDDNQFTDAGINTDNTYA 360
OY 361 LGIVYQF 367
DB 361 LGIVYQF 367
RESULT 2
ID OMPC_SALTI STANDARD; PRT; 378 AA.
AC P09878;
DT 01-MAR-1989 (rel. 10, Created)
DT 01-MAY-1991 (rel. 18, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC).
GN OMPC.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90060831; PubMed=2684785;
RA Puente J.L., Alvarez-Scherer V., Gosset G., Calva E.;
RT "Comparative analysis of the salmonella typhi and Escherichia coli
RT ompC genes."
RN Gene 83:197-206(1989).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88319959; PubMed=3412902;
RA Venegas A., Gomez I., Zaror I., Yudelevich A.;
RT "The nucleotide sequence of the salmonella typhi ompC porin gene."
RL Nucleic Acids Res. 16:7721-7721(1988).
RN [3]
RP 3D-STRUCTURE MODELING, AND CRYSTALLIZATION.
RX MEDLINE=99332091; PubMed=10405180;
RA Arockiasamy A., Krishnaswamy S.;
RT "Crystallization of the immunodominant outer membrane protein OmpC;
RT the first protein crystals from Salmonella typhi, a human pathogen."
RL FEBS Lett. 453:380-382(1999).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHO FAMILY OF PORINS.
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CC -----
DR EMBL: M31424; AAA27169.1; -
DR EMBL: X07835; CAA30688.1; -

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AC 052503;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC).
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_Taxid=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14028;
RA Negm R.S., Pistole T.G.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC -----
DR EMBL; AF039309; AAB96675.1; -.
DR StyrGene; SG10675; OMPC.
DR InterPro; IPR001702; -.
DR InterPro; IPR001897; -.
DR Pfam; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLIMPORIN.
DR PRINTS; PR00183; ECOLIMPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 1 21 OUTER MEMBRANE PROTEIN C.
SQ SEQUENCE 378 AA; 41299 MW; FC294209A91D79FA CRC64;

Query Match 77.4%; Score 1512.5; DB 1; Length 378;
Best Local Similarity 76.6%; Pred. No. 5.2e-98;
Matches 294; Conservative 26; Mismatches 41; Indels 23; Gaps 6;

QY 1 MKSKVALALIPALLAAGAAHAAEVYKKDKNKLDLYGKVDGLHFFSDNKKVDGDDQTYMRIG 60
DB 1 MKKRVATLIPALLAAGAAHAAEVYKKDKNKLDLYGKVDGLHFFSDNKKVDGDDQTYMRIG 60
QY 61 FKGETVDTQLTGYGMEYOIOGNSAENENNSWTRVAFAGLKFQDVGSEFDYGRNYYV 120
DB 61 FKGETVDTQLTGYGMEYOIOGNSAENENNSWTRVAFAGLKFQDVGSEFDYGRNYYV 120
QY 121 VTSWTDVLPFEGGDTYGSNFMQGRNFGATYRNTEFFGLYVDGLNFAVYOYQKNGNPSGE 180
DB 121 VTSWTDVLPFEGGDTYGSNFMQGRNFGATYRNTEFFGLYVDGLNFAVYOYQKNGNPSGE 180
QY 121 VTSWTDVLPFEGGDTYGSNFMQGRNFGATYRNTEFFGLYVDGLNFAVYOYQKNGNPSGE 180
DB 121 VTSWTDVLPFEGGDTYGSNFMQGRNFGATYRNTEFFGLYVDGLNFAVYOYQKNGNPSGE 180
QY 181 GFTSGVTNNGRDALRQNGDVGGSITTYD-EGFGIGCAISSSKRT-DAQNT-AAVIGNG 236
DB 181 GFTSGVTNNGRDALRQNGDVGGSITTYD-EGFGIGCAISSSKRT-DAQNT-AAVIGNG 236
QY 181 GFTSGVTNNGRDALRQNGDVGGSITTYD-EGFGIGCAISSSKRT-DAQNT-AAVIGNG 236
DB 181 GFTSGVTNNGRDALRQNGDVGGSITTYD-EGFGIGCAISSSKRT-DAQNT-AAVIGNG 236
QY 237 DRAETTYTGGLKTDANNIYLAAYQTYOTYNAATRVG-----SLGNAKAQNEFAVAQIQ 287
DB 237 DRAETTYTGGLKTDANNIYLAAYQTYOTYNAATRVG-----SLGNAKAQNEFAVAQIQ 287
QY 235 DRAETTYTGGLKTDANNIYLAAYQTYOTYNAATRVG-----SLGNAKAQNEFAVAQIQ 294
DB 235 DRAETTYTGGLKTDANNIYLAAYQTYOTYNAATRVG-----SLGNAKAQNEFAVAQIQ 294
QY 288 FDEGLRPSLAAYLOSKGKNTLGRG-----YDDEDDILKYVDVGYATYFNKMSGYVDYKINLDD 343
DB 288 FDEGLRPSLAAYLOSKGKNTLGRG-----YDDEDDILKYVDVGYATYFNKMSGYVDYKINLDD 343
QY 295 FDEGLRPSLAAYLOSKGKNTLGRG-----YDDEDDILKYVDVGYATYFNKMSGYVDYKINLDD 354
DB 295 FDEGLRPSLAAYLOSKGKNTLGRG-----YDDEDDILKYVDVGYATYFNKMSGYVDYKINLDD 354
QY 344 DNGFTDAGINTDNIVALGLVYOF 367
DB 344 DNGFTDAGINTDNIVALGLVYOF 367

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DB 355 KYEFTDAGINTDNIVALGLVYOF 378

RESULT 5
ID OMS2_SALT1 STANDARD; PRT; 383 AA.
AC 056111;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN S2 PRECURSOR.
GN OMP52.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_Taxid=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JMS-1;
RA Fernandez-Mora M., Calva E.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -----
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CC -----
DR EMBL; X89756; CA61903.1; -.
DR InterPro; IPR001702; -.
DR InterPro; IPR001897; -.
DR Pfam; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLIMPORIN.
DR PRINTS; PR00183; ECOLIMPORIN.
DR Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 1 21 OUTER MEMBRANE PROTEIN S2.
SQ SEQUENCE 383 AA; 42183 MW; 47CFB6B5F6A2370F CRC64;

Query Match 66.4%; Score 1296; DB 1; Length 383;
Best Local Similarity 66.8%; Pred. No. 5.3e-83;
Matches 256; Conservative 37; Mismatches 74; Indels 16; Gaps 8;

QY 1 MKSKVALALIPALLAAGAAHAAEVYKKDKNKLDLYGKVDGLHFFSDNKKVDGDDQTYMRIG 60
DB 1 MKKRVATLIPALLAAGAAHAAEVYKKDKNKLDLYGKVDGLHFFSDNKKVDGDDQTYMRIG 60
QY 61 FKGETVDTQLTGYGMEYOIOGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNYYV 119
DB 61 FKGETVDTQLTGYGMEYOIOGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNYYV 119
QY 61 FKGETVDTQLTGYGMEYOIOGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNYYV 119
DB 61 FKGETVDTQLTGYGMEYOIOGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNYYV 119
QY 120 DYSWTDVLPFEGGDTYGSNFMQGRNFGATYRNTEFFGLYVDGLNFAVYOYQKNGNPS 178
DB 120 DYSWTDVLPFEGGDTYGSNFMQGRNFGATYRNTEFFGLYVDGLNFAVYOYQKNGNPS 178
QY 121 DVEGTDMLPEFGGDSYTAADNYMTGRANGVATYRNTEFFGLYVDGLNFAVYOYQKNGN 180
DB 121 DVEGTDMLPEFGGDSYTAADNYMTGRANGVATYRNTEFFGLYVDGLNFAVYOYQKNGN 180
QY 179 GEGFTSGVT--NNGRDALRQNGDVGGSITTYD-EGFGIGCAISSSKRTDAQ-NNAAYIG 234
DB 179 GEGFTSGVT--NNGRDALRQNGDVGGSITTYD-EGFGIGCAISSSKRTDAQ-NNAAYIG 234
QY 181 ADDVNTGTTNRRNGDDIRVNDGDFGISTTYDYGFGSAGAAVTSYSDRTNEGVNAGCTTA 240
DB 181 ADDVNTGTTNRRNGDDIRVNDGDFGISTTYDYGFGSAGAAVTSYSDRTNEGVNAGCTTA 240
QY 235 NCDRAETTYTGGLKTDANNIYLAAYQTYOTYNAATRVSL-----GNANKAQNFEAQAQYOF 288
DB 235 NCDRAETTYTGGLKTDANNIYLAAYQTYOTYNAATRVSL-----GNANKAQNFEAQAQYOF 288
QY 241 GGDKADAMTAGLKYDANNIYLAAYQTYOTYNAATRVSL-----GNANKAQNFEAQAQYOF 300
DB 241 GGDKADAMTAGLKYDANNIYLAAYQTYOTYNAATRVSL-----GNANKAQNFEAQAQYOF 300
QY 289 DFGRLPSLAAYLOSKGKNTLGRG-----GRGYDDEDDILKYVDVGYATYFNKMSGYVDYKINLDDN 345
DB 289 DFGRLPSLAAYLOSKGKNTLGRG-----GRGYDDEDDILKYVDVGYATYFNKMSGYVDYKINLDDN 345
QY 301 DGLRPAVAFSLMSKGLTYNNVNGDDKDLVYKADVGYATYFNKMSGYVDYKINLDDDD 360
DB 301 DGLRPAVAFSLMSKGLTYNNVNGDDKDLVYKADVGYATYFNKMSGYVDYKINLDDDD 360

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QY 346 Q-ETRDAGINTDNIVALGLVYQF 367
 ID :||||:||||:||||:
 Db 361 DPEYKDGISTDIDVALGMVYQF 383

RESULT 6
OMPN.ECOLI

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sampaio G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).

RP SEQUENCE FROM N.A., SEQUENCE OF 22-33. AND CHARACTERIZATION.
 RX MEDLINE=98317278; PubMed=9642192;
 RA Prilipov A., Phale P.S., Koehn R., Widmer C., Rosenbusch J.P.;
 RT "Identification and characterization of two quiescent porin genes,
 RT ompC and ompN, in Escherichia coli BE.";
 RL J. Bacteriol. 180:3388-3392(1998).
 CC -1- FUNCTION: NON-SPECIFIC PORIN.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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 CC -----
 CC EMBL; AB000234; AAC74459.1; -
 CC EMBL; D90775; BAA14981.1; -
 CC EMBL; D90776; BAA14986.1; -
 CC Ecocore; BGL3375; ompN.
 CC InterPro; IPR001702; -
 CC InterPro; IPR001897; -
 CC Pfam; PF00267; Gram-ve_porins; 1.
 CC PRINTS; PR00182; ECOLNIPORIN.
 CC PRINTS; PR00183; ECOLIPORIN.
 CC Outer membrane; Transmembrane; Porin; Signal.
 FT SIGNAL 1 21

FT CHAIN 22 377 OUTER MEMBRANE PROTEIN N.
 SQ SEQUENCE 377 AA; 41220 MW; 4420D2CB9BC10F95 CRC64;

Query Match 66.3%; Score 1295; DB 1; Length 377;
 Best Local Similarity 67.8%; Pred. No. 6, 1e-83;
 Matches 261; Conservative 37; Mismatches 61; Indels 26; Gaps 10;

QY 1 MRSKVALLIPALLAAGAAHAAEVYNNKDKLDLYKVDGLHFEFSNNKDVDPQTYMRIG 60
 Db 1 MRSKVALLIPALLAAGAAHAAEVYNNKDKLDLYKVDGLHFEFSNNKDKQSGSTARIG 60
 QY 61 FKEGTVDQLDLYGQWEXQIQGNSAE--NENSWTVAFAGLKDQVGSFDYGRNAYV 119
 Db 61 FKEGTVDQLDLYGQWEXYIQANTESSKNQSWTBLAFGLKFAFDYGSFDYGRNAYV 120
 QY 120 DVTSWMDVLPFGGDRY--GSDNFMQORNGFARYRTDFGLVDGLNFAVQYGRKNGNS 178
 Db 121 DLGWTMDLPFGGDSYTNADNMTGRANGVATYRNTDFGLVNGINFAVQYQGN-- 176
 QY 179 GEGFTSGV--TNNGRDLNONGDVGSGITYDY--EGFGIGATISSKRIDAQ--NTAAYI 233
 Db 177 -EGASNGEGTNGRVRHENGNGMGLSTTYDGMGFSAGAATSSDRNDQVNHAA-- 233
 QY 234 GNGDRAEYTYGKDYDANNIYLAAYTYQYNAIVRSLGW--ANKAQNFAVAQYQDFG 291
 Db 234 -GGDKADMTAGLKDYDANNIYLAATMYSETRNMTPFGDSVAIVANKTQNEFVTAQYQDFG 292
 QY 292 LRSLAVLYOSKGNL-----GRYDEDEDLYKYDVATYFNNKMSYVDYKINLID 343
 Db 293 LRPAVSFLMSKGRDLHAAGADNPAGVDKLVKADIGATYTFNNKMSYVDYKINLID 352
 QY 344 -DNOETRDAGINTDNIVALGLVYQF 367
 Db 353 EDDSFYAANGISTDIDVALGLVYQF 377

RESULT 7
OMPC.SERMA

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-UOC-51;
 RX MEDLINE=94236242; PubMed=8180703;
 RA Hutsul J.A.W., Worobec E.A.;
 RT "Molecular characterization of a 40 kDa OmpC-like porin from Serratia
 RT marcescens.";
 RL Microbiology 140:379-387(1994).

CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
 CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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 CC -----
 CC EMBL; L24960; AAA26562.1; -
 CC

```

DR InterPro: IPR001702; -.
DR InterPro: IPR001897; -.
DR Pfam: PF00267; Gram-ve porins; 1.
DR PRINTS: PRO0182; ECOLIPORIN.
DR PRINTS: PRO0183; ECOLIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
DR Outer membrane: Transmembrane; Porin; Phase recognition; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 376 OUTER MEMBRANE PROTEIN C.
SQ SEQUENCE 376 AA: 41440 MW: 81227FE851B568E CRC64;

Query Match 65.7%; Score 1283.5; DB 1; Length 376;
Best local Similarity 65.6%; Pred. No. 3.8e-82;
Matches 252; Conservative 48; Mismatches 59; Indels 25; Gaps 8;

QY 1 MRSKVALALIPALLAGAAHAAEYNNKDKGKLDLYGKVDGLHFSDNKDYDQOTYRRLG 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 MKRLVSLAVPALIVAGTAGAAETYNKDKGKLDLYGKVDLHFSNNGYDGDQSYRFG 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 FKGETOVTDLTGYGOMEXYIOGNSAENENN-SMTRYAFAGLKFODYGSFDYGRNYGVY 119
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 61 LRETOISDQLTGYGOMEXYIOGNSAENENN-SMTRYAFAGLKFODYGSFDYGRNYGVY 120
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 DVTSMVDVLPFGGDTYGSDFNQQRNFGATYRNTDFGLVDGLNFAVOYQKNGPSC 179
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 121 DVAATYDLQEPFGDMYTGADQFMFQSRSSGLATYRNDFGLVDGLNFAVOYQKNGN -G 178
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 180 EGTSGVTNNGRALRQNGCGVGSITYDEEGFI--GGAISSKRTDAONTA----AYI 233
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 179 E-----ETNNGRYVLQONGEGYMSMSYDM-GYGISAAAFENSRRTSEONGAHONIM 232
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 234 GNDRAETYGGLKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAQNFEAVAOYOF 288
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 233 GRDKAKAGYGGGLKYDANNIYLAAMFTQSTNARFGSSDSYVGYANKAOSPERYAHYOF 292
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 289 DFGLRPSLAYLQSGKKNLGRG---YDDEDLIKYVDVGYATYFNKMSYVDYKINLMD 343
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 293 DFGLRPEVYNGTKRKQDLGRAGNKGKQDGLVDFGLGATYFNKMSYVDYKINLMD 352
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 344 DNOFTDRAGINTDNIVYALGLVYOF 367
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 353 NNDFTDAGINTDNIVYALGLVYOF 376
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
OMPF_SERMA STANDARD: PRT; 374 AA.
AC 033960;
DB 15-DEC-1998 (Rel. 37, Created)
DB 15-DEC-1998 (Rel. 37, Last sequence update)
DB 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF).
GN OMPF.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBL_Taxid=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UOC-51;
RX MEDLINE-97419518; PubMed-9274033;
RA Hutsul J.A.M., Worobec E.A.;
RT "Molecular characterization of the Serratia marcescens OmpF porin,
and analysis of S. marcescens OmpF and OmpC osmoregulation.";
RL Microbiology 143:2797-2806(1997).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPF/PHOE FAMILY OF PORINS.
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CC -----
DR EMBL: U81967; AAB69103.1; AUT_INIT.
DR InterPro: IPR001702; -.
DR InterPro: IPR001897; -.
DR Pfam: PF00267; Gram-ve porins; 1.
DR PRINTS: PRO0182; ECOLIPORIN.
DR PRINTS: PRO0183; ECOLIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
DR Outer membrane: Transmembrane; Porin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 374 OUTER MEMBRANE PROTEIN F.
SQ SEQUENCE 374 AA: 41184 MW: BF821D385E441049 CRC64;

Query Match 63.5%; Score 1241; DB 1; Length 374;
Best local Similarity 64.3%; Pred. No. 3.3e-79;
Matches 249; Conservative 36; Mismatches 68; Indels 34; Gaps 8;

QY 1 MRSKVALALIPALLAGAAHAAEYNNKDKGKLDLYGKVDGLHFSDNKDYDQOTYRRLG 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 2 MKNRIILAVVIPALLAGAAHAAEYNNKDKGKLDLYGKVDLHFSKDKNDGQOTYVRF 61
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 FKGETOVTDLTGYGOMEXYIOGNSAENE--NNSMTRYAFAGLKFODYGSFDYGRNYGVY 118
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 62 FKGETOITDQLTGYGOMEXYIOGNSAENESQETKTRRLGAGLKFADYGSFDYGRNYGVY 121
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 YDVTSMVDVLPFGGDTYGSDFNQQRNFGATYRNTDFGLVDGLNFAVOYQKNGNP 177
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 122 YDVEGMDMLPEFGDTYGSDFNQQRNFGATYRNTDFGLVDGLNFAVOYQKNGN --- 178
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 178 SGCGFTSGVTNNGRALRQNGCGVGSITYDY-EGGIGALISSKRTDAONTAAIYNG 236
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 179 -----ONDRDYKQKONGDWGJISITYDEGVSPGAAVASSNRTPDOKLRN-ERG 228
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 237 DRAETYGGLKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAQNFEAV 283
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 229 DKADANTVGAKYDANNIYLAAMTAETRNMTFFGCGNFTNTCAATENGCGFASTQTFEY 288
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 284 AOYQDFGRLPSLAYLQSGKKNL---GRGYDDEDLIKYVDVGYATYFNKMSYVDYKIN 340
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 289 AOYQDFGRLPEVSYLQSGKKNLNVPGVG--SDQDLKVVSVGYTYFNKMSYVDYKIN 347
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 341 LDDNOFTDRAGINTDNIVYALGLVYOF 367
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 348 LDDNDFTRAGIATDIDVGVGLVYOF 374
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 9
OMPC_BAHQ STANDARD: PRT; 342 AA.
AC 033507;
DB 15-DEC-1998 (Rel. 37, Created)
DB 15-DEC-1998 (Rel. 37, Last sequence update)
DB 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN C (PORIN OMPC) (FRAGMENT).
GN OMPC.
OS Rahmella aquatilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Rahmella.
OX NCBL_Taxid=34038;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CF3;
RX MEDLINE-98132388; PubMed-9473046;
RA Achouak W., Pages J.M., de Mot R., Mollé G., Heulin T.;
RT "A major outer membrane protein of Rahmella aquatilis functions as a
porin and root adhesin.";
RL J. Bacteriol. 180:909-913(1998).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR

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CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC IN R.AQATLIS OMPc IS INVOLVED IN THE ADHESION TO WHEAT ROOTS.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPc/PHOE FAMILY OF PORINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ002879; CA05726.1; -.
CC InterPro: IPR001702; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC Outer membrane; Transmembrane; Porin.
CC NON_TER 1 342 1
CC FT 342 342
CC SEQUENCE 342 AA; 37674 MW; 5B60D8FA5AD977A5 CRC64;

Query Match 62.5%; Score 1220; DB 1; Length 342;
Best Local Similarity 67.5%; Pred. No. 8.5e-78;
Matches 237; Conservative 43; Mismatches 51; Indels 20; Gaps 7;

QY 23 EVNKGDKNKLIDLGKVDGLHFSNDKVDGDQTYMRGLGFKGQVNTDOLGYGOMERYQ 82
   1 EYNNKDKNKLIDLGKVDGLHFSNDKVDGDQTYMRGLGFKGQVNTDOLGYGOMERYQ 82
Db 1 EYNNKDKNKLIDLGKVDGLHFSNDKVDGDQTYMRGLGFKGQVNTDOLGYGOMERYQ 82
QY 83 GNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNVGVYDVTSMTDVLPEFGDTYGS 141
   1 LNTAESDANENFTRVAGLKFQDVGSEFDYGRNVGVYDVTSMTDVLPEFGDTYGS 141
Db 1 LNTAESDANENFTRVAGLKFQDVGSEFDYGRNVGVYDVTSMTDVLPEFGDTYGS 141
QY 142 MOORNGNATRYRTDFEGLVDGLNFAVQYQKNGNPSGEFTSGVTNNGDALRQNGDV 201
   1 MFRPANGVLTYYRNKDFEGLVDGLNFAVQYQKNGNPSGEFTSGVTNNGDALRQNGDV 201
Db 1 MFRPANGVLTYYRNKDFEGLVDGLNFAVQYQKNGNPSGEFTSGVTNNGDALRQNGDV 201
QY 121 MFRPANGVLTYYRNKDFEGLVDGLNFAVQYQKNGNPSGEFTSGVTNNGDALRQNGDV 173
   1 MFRPANGVLTYYRNKDFEGLVDGLNFAVQYQKNGNPSGEFTSGVTNNGDALRQNGDV 173
Db 1 MFRPANGVLTYYRNKDFEGLVDGLNFAVQYQKNGNPSGEFTSGVTNNGDALRQNGDV 173
QY 202 GGSITVDY-EGFGIGAISSSKRTDAQ--TAAYIGNGDRAETYGGLKYDNNIYLA 257
   1 GGSITVDY-EGFGIGAISSSKRTDAQ--TAAYIGNGDRAETYGGLKYDNNIYLA 257
Db 1 GGSITVDY-EGFGIGAISSSKRTDAQ--TAAYIGNGDRAETYGGLKYDNNIYLA 257
QY 174 GMSLTVDLGSGFSAAGAMASTRTSEONGRQNPAILIGNDRAETYGGLKYDNNIYLA 233
   1 GMSLTVDLGSGFSAAGAMASTRTSEONGRQNPAILIGNDRAETYGGLKYDNNIYLA 233
Db 1 GMSLTVDLGSGFSAAGAMASTRTSEONGRQNPAILIGNDRAETYGGLKYDNNIYLA 233
QY 258 QYQTYNATRYG-----SLGMANKQNFPAVAQYQDFGLRPSLAVYQKNGRQNG 311
   1 QYQTYNATRYG-----SLGMANKQNFPAVAQYQDFGLRPSLAVYQKNGRQNG 311
Db 1 QYQTYNATRYG-----SLGMANKQNFPAVAQYQDFGLRPSLAVYQKNGRQNG 311
QY 234 VFGQTYNA-RIGVSSDSHSHGYADNAQNFPAVAQYQDFGLRPSLAVYQSHARNV-PGYS 291
   1 VFGQTYNA-RIGVSSDSHSHGYADNAQNFPAVAQYQDFGLRPSLAVYQSHARNV-PGYS 291
Db 1 VFGQTYNA-RIGVSSDSHSHGYADNAQNFPAVAQYQDFGLRPSLAVYQSHARNV-PGYS 291
QY 312 DEDILKYVDVGATYYRNKMSITYVDKINLLDNOFTROAGITDNIYALG 362
   1 DEDILKYVDVGATYYRNKMSITYVDKINLLDNOFTROAGITDNIYALG 362
Db 1 DEDILKYVDVGATYYRNKMSITYVDKINLLDNOFTROAGITDNIYALG 362
QY 292 NQMLTYVDVGASYFNNKMLTYVDKINLLDNOFTROAGITDNIYALG 342
   1 NQMLTYVDVGASYFNNKMLTYVDKINLLDNOFTROAGITDNIYALG 342
Db 1 NQMLTYVDVGASYFNNKMLTYVDKINLLDNOFTROAGITDNIYALG 342

RESULT 10
OMSL_SALTI STANDARD; PRT; 394 AA.
AC Q56110;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN S1 PRECURSOR.
GN OMPs1.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMSS-1;
RA MEDLINE=95309727; PubMed=7769812;
RA Fernandez-Mora M., Oropeza R., Puente J.L., Calva E.;
RT Isolation and characterization of ompS1, a novel Salmonella typhi
RT outer membrane protein-encoding gene.";
RL Gene 158:67-72(1995).

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CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE OMPc/PHOE FAMILY OF PORINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X73237; CAAS1710.1; -.
CC InterPro: IPR001702; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC PRINTS: PR00183; ECOLIPORIN.
CC PRINTS: PR00183; ECOLIPORIN.
CC PROSITE: PS00576; GRAM_NEG_PORIN; 1.
CC Signal; Outer membrane; Transmembrane; Porin.
CC SIGNAL 1 21
CC FT 22 394
CC CHAIN 1 21
CC SEQUENCE 394 AA; 43253 MW; E7C8FEED424931D1 CRC64;

Query Match 62.1%; Score 1213.5; DB 1; Length 394;
Best Local Similarity 62.8%; Pred. No. 2.8e-77;
Matches 248; Conservative 38; Mismatches 80; Indels 29; Gaps 10;

QY 1 MRSKVALALIPALLAAGAAHAFAVYNNKDKNKLIDLYGKVDGLHFSNDKVDGDQTYMR 60
   1 MNRKVALALIPALLAAGAAHAFAVYNNKDKNKLIDLYGKVDGLHFSNDKVDGDQTYMR 60
Db 1 MNRKVALALIPALLAAGAAHAFAVYNNKDKNKLIDLYGKVDGLHFSNDKVDGDQTYMR 60
QY 61 FKGETVDTQDLTGSGOMERYIQGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNV 119
   1 FKGETVDTQDLTGSGOMERYIQGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNV 119
Db 1 FKGETVDTQDLTGSGOMERYIQGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNV 119
QY 61 FKGETVDTQDLTGSGOMERYIQGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNV 120
   1 FKGETVDTQDLTGSGOMERYIQGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNV 120
Db 1 FKGETVDTQDLTGSGOMERYIQGNSAENEN-NSWTRVAFAGLKFQDVGSEFDYGRNV 120
QY 120 DVTSMWTDVLPFEGDITY-GSDNFMQORGNFATRYRTDFEGLVDGLNFAVQYQKNGNPS 178
   1 DVTSMWTDVLPFEGDITY-GSDNFMQORGNFATRYRTDFEGLVDGLNFAVQYQKNGNPS 178
Db 1 DVTSMWTDVLPFEGDITY-GSDNFMQORGNFATRYRTDFEGLVDGLNFAVQYQKNGNPS 178
QY 121 DIAMWDALPEFGDITYQDYVNLGRTNGVATRYRTDFEGLVDGLNFAVQYQKNGNEN-G 179
   1 DIAMWDALPEFGDITYQDYVNLGRTNGVATRYRTDFEGLVDGLNFAVQYQKNGNEN-G 179
Db 1 DIAMWDALPEFGDITYQDYVNLGRTNGVATRYRTDFEGLVDGLNFAVQYQKNGNEN-G 179
QY 179 GEGFTSGVTNNG-RDALRQNGDVGSGITYDY-EGFGIGAISSSKRTDAQNTAA- 232
   1 GEGFTSGVTNNG-RDALRQNGDVGSGITYDY-EGFGIGAISSSKRTDAQNTAA- 232
Db 1 GEGFTSGVTNNG-RDALRQNGDVGSGITYDY-EGFGIGAISSSKRTDAQNTAA- 232
QY 180 GAGAGSGTGGNGRKLARENGDEGMSYSTDFEGLSLGAAYSSSDSNQVARGYGDGM 239
   1 GAGAGSGTGGNGRKLARENGDEGMSYSTDFEGLSLGAAYSSSDSNQVARGYGDGM 239
Db 1 GAGAGSGTGGNGRKLARENGDEGMSYSTDFEGLSLGAAYSSSDSNQVARGYGDGM 239
QY 233 -----IGNDRAETYGGLKYDANNIYLAQYQTYNATRYG-----GSLGMANKQNF 281
   1 -----IGNDRAETYGGLKYDANNIYLAQYQTYNATRYG-----GSLGMANKQNF 281
Db 1 -----IGNDRAETYGGLKYDANNIYLAQYQTYNATRYG-----GSLGMANKQNF 281
QY 240 NERNNTYAGGETAFAWTGATYDAVNYLAAMVATRYRTMYGGGNGBGNGSIANKTONFE 299
   1 NERNNTYAGGETAFAWTGATYDAVNYLAAMVATRYRTMYGGGNGBGNGSIANKTONFE 299
Db 1 NERNNTYAGGETAFAWTGATYDAVNYLAAMVATRYRTMYGGGNGBGNGSIANKTONFE 299
QY 282 AVAQYQDFGLRPSLAVYQKNGRQNG-----RG-----YDDEDILKYVDVGATYYFNKRMST 333
   1 AVAQYQDFGLRPSLAVYQKNGRQNG-----RG-----YDDEDILKYVDVGATYYFNKRMST 333
Db 1 AVAQYQDFGLRPSLAVYQKNGRQNG-----RG-----YDDEDILKYVDVGATYYFNKRMST 333
QY 300 VVAQYQDFGLRPSLAVYQKNGRQNGDGLGQEVHNRGNWRYTDKDLVYQGVGTYTFNNKMS 359
   1 VVAQYQDFGLRPSLAVYQKNGRQNGDGLGQEVHNRGNWRYTDKDLVYQGVGTYTFNNKMS 359
Db 1 VVAQYQDFGLRPSLAVYQKNGRQNGDGLGQEVHNRGNWRYTDKDLVYQGVGTYTFNNKMS 359
QY 334 YVDKINLLD-DNQFTROAGITDNIYALGLVYQF 367
   1 YVDKINLLD-DNQFTROAGITDNIYALGLVYQF 367
Db 1 YVDKINLLD-DNQFTROAGITDNIYALGLVYQF 367
QY 360 YVDKINLLDDEDDFYANNNGIATDITVGLVYQF 394
   1 YVDKINLLDDEDDFYANNNGIATDITVGLVYQF 394
Db 1 YVDKINLLDDEDDFYANNNGIATDITVGLVYQF 394

RESULT 11
YEDS_ECOLI STANDARD; PRT; 397 AA.
AC P76335; O07986; P76336; P94747; P94748;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTENTIAL OUTER MEMBRANE PROTEIN YEDS PRECURSOR.
GN YEDS OR B1964/B1965/B1966.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562.
RN [1]

```

RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-97251358; PubMed-9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
 RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
 RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
 RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,
 RA Yamamoto Y., Horinouchi T.;
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 40,1-50,0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 RN [3]
 RP CONCEPTUAL TRANSLATION.
 RA Rudd K.E.;
 RC Unpublished observations (JUN-1998).
 RL -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE OMP/POE FAMILY OF PORINS.
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION. AN IN-FRAME STOP CODON
 WAS READ OVER IN POSITION 162 AND TWO POTENTIAL FRAMESHIFTS WERE
 CORRECTED.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE000288; AAC75030.1; ALT_FRAME.
 DR EMBL: AE000288; AAC75031.1; ALT_FRAME.
 DR EMBL: AE000288; AAC75032.1; ALT_FRAME.
 DR EMBL: D90835; BAA15791.1; ALT_FRAME.
 DR EMBL: D90835; BAA15792.1; ALT_FRAME.
 DR EMBL: D90835; BAA15793.1; ALT_FRAME.
 DR EcoGene: EGI4042; yedS.
 DR InterPro: IPR001702; -.
 DR InterPro: IPR001897; -.
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLNEIPORIN.
 DR PRINTS: PR00183; ECOLIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Hypothetical protein; Outer membrane; Transmembrane; Porin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 397 POTENTIAL. OUTER MEMBRANE PROTEIN YEDS.
 SQ SEQUENCE 397 AA; 42981 MW; 9C5183E5432FE0F0 CRC64;

Query Match 60.8%; Score 1187; DB 1; Length 397;
 Best Local Similarity 61.0%; Pred. No. 1,9e-75;
 Matches 244; Conservative 41; Mismatches 79; Indels 36; Gaps 10;

QY 1 MKSVALLLPALLAAGAAHAAYNKDGNKLDYGVDELHFSDDKDVDSQDTYRLG 60
 DB 1 MKRVVLAIVPALVPAAGAAHAAYNKDGNKLDYGVDELHFSDDKDVDSQDTYRLG 60
 QY 61 FKGETVTDLTGAGGWEYOIOGNSAENE-NNSWTRVAFAGLKFQDVGSDYGRNGVYV 119
 DB 61 FKGETVTDLTGAGGWEYOIOGNSAENE-NNSWTRVAFAGLKFQDVGSDYGRNGVYV 120

QY 120 DVTSWTDVLEPEFGDITV-GSDNFMQQRGNFGATYRNTDFEGLVDGLNFAVYOYQGN--GN 176
 DB 121 DVEAWTMDLEPEFGDITVAGADNFMNRRANGVATYRNNGFFGXVDLNFALYOYQGNNSGC 180
 QY 177 PSG-EGFTSGVTNNGRALKRDGVCSTTYDYE-GFGIGAISSSKRPDAQ----- 227
 DB 181 PFQGGGSGSG---DGRSLSKENGDFGFMSTSYDFEGLSLGAAYXNDRSDRQVGLND 237
 QY 228 -NTAAVYIGNDRAPETVYGGKRDANNTYLAAYOTQYATNATRVGS-----LGMANKA 277
 DB 238 RNHSNRNAGGETAFATVYGAKYDANNVYLAAMYAETNNMTPYGGGEEDNESATANKT 297
 QY 278 QNFEAVALYOYDFEGLRPSLAYLQSKGNLG-----RGYDEDLIKYVDGATYFN 328
 DB 298 QNFEAVALYOYDFEGLRPSLAYLQSKGNLGMAHNGDPRPTNKLVDKYVDIGATYFN 357
 QY 329 KNNSTVYDYKINLND-DNQETRDAGITVDNIVAGLYYQF 367
 DB 358 KNNSTVYDYKINLNDNDEYFANGIATDIDIVAGLYYQF 397

RESULT 12

NMPC_ECOLI STANDARD; PRT; 365 AA.

AC P21420; P77189;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTER MEMBRANE PORIN PROTEIN NMPC PRECURSOR.
 GN NMPC OR PHMA.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MUTANT CS384;
 RX MEDLINE-86304457; PubMed-3017988;
 RA Blasband A.J., Marcotte W.R. Jr., Schnaitman C.A.;
 RT "Structure of the lc and nmcp outer membrane porin protein genes of
 RT *lambdaoid bacteriophage*.";
 RL J. Biol. Chem. 261:12723-12732(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.

RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
 RA Federspiel N., Hyman R., Kaiman S., Komp C., Kuri O., Lew H., Lin D.,
 RA Namach A., Oelner P., Roberts D., Schramm S., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 347-365 FROM N.A.
 RC STRAIN-J15502;
 RX MEDLINE-94335635; PubMed-8057841;
 RA Coll J.L., Heyde M., Portallier R.;
 RT "Expression of the nmcp gene of *Escherichia coli* K-12 is modulated by
 RT external pH. Identification of cis-acting regulatory sequences
 RT involved in this regulation.";
 RL Mol. Microbiol. 12:83-93(1994).
 RN [5]

RP SEQUENCE OF 347-365 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-96196428; PubMed-8648624;
 RA Mandl A.A., Sharples G.J., Mandal T.N., Lloyd R.G.;
 RT "Holliday junction resolvases encoded by homologous *rusA* genes in

```

RT Escherichia coli K-12 and phage 82."
RL J. Mol. Biol. 257:561-573(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC MISCELLANEOUS: IN WILD-TYPE STRAINS OF E. COLI K12, THE NMPC OPEN
CC READING FRAME IS INTERRUPTED BY AN ISS INSERTION AND GENERATES A
CC HYBRID OPEN READING FRAME THAT IS NOT EXPRESSED. HOWEVER, IN
CC MUTANT STRAIN CS348, THE ISS ELEMENT HAS BEEN DELETED AND NMPC IS
CC EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M13457; AAA33728.1; ALT_SEQ.
CC EMBL: AE000160; AAC73654.1; ALT_SEQ.
CC EMBL: U82598; AAB40749.1; ALT_SEQ.
CC EMBL: Z35442; CAA84594.1; -.
CC EMBL: X93587; CAA63325.1; -.
CC PIR: A25647; MMECNC.
CC HSSP: P02931; IGFN.
CC EcoGene: EGI0659; nmpc.
CC InterPro: IPR001702; -.
CC InterPro: IPR001897; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC PRINTS: PR00182; ECOLIPORIN.
CC PRINTS: PS00576; GRAM_NEG_PORIN; 1.
CC PROSITE: PS00183; ECOLIPORIN.
CC Outer membrane; Transmembrane; Porin; Signal.
CC SIGNAL 1 23
CC FT CHAIN 24 365 OUTER MEMBRANE PORIN PROTEIN NMPC.
CC FT CONFLICT 326 326 K -> N (IN REF. 2 AND 3).
CC FT SEQUENCE 365 AA; 40316 MW; 6E5128D4847FBAF8 CRC64;
CC -----
Query Match 60.3%; Score 1177; DB 1; Length 365;
Best Local Similarity 62.1%; Pred. No. 8.7e-75;
Matches 234; Conservative 41; Mismatches 80; Indels 22; Gaps 6;
QY 1 MRSKVAL--LIPALLAAGAAHAAYVYKDKGKLDLYGKVDGLHYPSDNKDVGDQTYMR 58
DB 1 MKRLTVAISAVAASVLAAMSQAQAEIYNKDSNKLIDYGVNAKHFFSSNADGDTTYAR 60
QY 59 LGRKGETOVDTLGTGOWEYQIOGNSAENENNS--WTRVAFGLKFDVGSFDYGRNYG 116
DB 61 LGRKGETOINDOLGTGOWEYEFKGNRAESQSSKDKTRLAFGLKFGDYSIDYGRNYG 120
QY 117 VVYDVTSMTDVLPEFGDITV--GSDNFMQORGNGFATYRNTPDFGLVDGLNFAVQYQKNG 175
DB 121 VAYDIGAMFTDVLPEFGDITVQTDVFTGRTGFATYRNNDPFGGLVDGLNFAVQYQKND 180
QY 176 NPSGEGFTSVTNNGRDALQNGDVGSGSTIYDEEGFGIGALSSSKRTDAONTAAYI-- 233
DB 181 RSPDNDYTES-----NCGDGFCSATYVEEGFGIGATYAKSDRPTQYVNAQVLP 229
QY 234 ---GNGRAETIYGLKYDANNITYLAQTYOTYATRVGSLGNAKNAKQNEAQAQYQDF 290
DB 230 EVFASGAGNAVAAGLKYDANNITYLATYSETQNTVFAADHFAVANKQNEAQAQYQDF 289
QY 291 GLRPSLAYLQSKSKNLGRGVEDILKYVVGATYVYFNKNNSTYVDYKINLLDNDQPTRD 350
DB 290 GLRPSAYLQSKGRDLG--VAGDDDLVYVVGATYVYFKKNNSTFYVDYKINLLDKNDPTKA 348
QY 351 AGINTDNIYALGLYQF 367
DB 349 LGVSTDDIVAAGLYQF 365
RESULT 13

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PORT_BPPA2
ID PORT_BPPA2 STANDARD; PRT; 365 AA.
AC P07238;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PORIN PROTEIN LC PRECURSOR.
GN LC.
OS Bacteriophage PA-2.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
OX NCBI_TaxID=10738;
RN (1)
RP SEQUENCE FROM N.A.
RA Blassland A.J., Marcotte W.R. Jr., Schaltman C.A.;
RX Medline=86304457; Pubmed=3017988;
RT "Structure of the lc and nmpc outer membrane porin protein genes of
RT lambdaoid bacteriophage."
RL J. Biol. Chem. 261:12723-12732(1986).
CC -1- FUNCTION: PORINS ARE MAJOR PROTEINS FOUND IN THE OUTER MEMBRANES
CC OF GRAM-NEGATIVE BACTERIA WHERE THEY FORM CHANNELS FOR THE
CC NONSPECIFIC PERMEATION OF SMALL SOLUTES (MOLECULES WITH MW LOWER
CC THAN 4000-6000 DALTONS).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J02580; AAA32301.1; -.
CC PIR: D25647; MMBP2.
CC HSSP: P02931; IGFN.
CC InterPro: IPR001702; -.
CC InterPro: IPR001897; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC PRINTS: PR00182; ECOLIPORIN.
CC PRINTS: PR00183; ECOLIPORIN.
CC PROSITE: PS00576; GRAM_NEG_PORIN; 1.
CC Outer membrane; Transmembrane; Porin; Signal.
CC SIGNAL 1 23
CC FT CHAIN 24 365 OUTER MEMBRANE PORIN PROTEIN LC.
CC FT CONFLICT 99 99 H -> R (IN AA SEQUENCE).
CC FT SEQUENCE 365 AA; 40290 MW; 0FB0C531FB9C0205 CRC64;
CC -----
Query Match 59.9%; Score 1169; DB 1; Length 365;
Best Local Similarity 61.8%; Pred. No. 3.1e-74;
Matches 233; Conservative 41; Mismatches 81; Indels 22; Gaps 6;
QY 1 MRSKVAL--LIPALLAAGAAHAAYVYKDKGKLDLYGKVDGLHYPSDNKDVGDQTYMR 58
DB 1 MKRLTVAISAVAASVLAAMSQAQAEIYNKDSNKLIDYGVNAKHFFSSNADGDTTYAR 60
QY 59 LGRKGETOVDTLGTGOWEYQIOGNSAENENNS--WTRVAFGLKFDVGSFDYGRNYG 116
DB 61 LGRKGETOINDOLGTGOWEYEFKGNRAESQSSKDKTRLAFGLKFGDYSIDYGRNYG 120
QY 117 VVYDVTSMTDVLPEFGDITV--GSDNFMQORGNGFATYRNTPDFGLVDGLNFAVQYQKNG 175
DB 121 VAYDIGAMFTDVLPEFGDITVQTDVFTGRTGFATYRNNDPFGGLVDGLNFAVQYQKND 180
QY 176 NPSGEGFTSVTNNGRDALQNGDVGSGSTIYDEEGFGIGALSSSKRTDAONTAAYI-- 233

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RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE-84297232; PubMed-6089111;
 RA Deutch A.H., Rushlow K.E., Smith C.J.;
 RT "Analysis of the Escherichia coli probA locus by DNA and protein
 sequencing.";
 RL Nucleic Acids Res. 12:6337-6355(1984).
 RN [6]
 RP MUTAGENESIS OF PHE-351.
 RX MEDLINE-91162638; PubMed-1848301;
 RA Struyve M., Moons M., Tommassen J.;
 RT "Carboxy-terminal phenylalanine is essential for the correct assembly
 of a bacterial outer membrane protein.";
 RL J. Mol. Biol. 218:141-148(1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (6.0 ANGSTROMS).
 RX MEDLINE-91172301; PubMed-1848682;
 RA Jap B.K., Wallan P.J., Gehring K.;
 RT "Structural architecture of an outer membrane channel as determined
 by electron crystallography.";
 RL Nature 350:167-170(1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE-92375189; PubMed-1380671;
 RA Cowan S.W., Schirmer T., Rummel G., Steiert M., Ghosh R.,
 RA Paupert R.A., Jansons J.N., Rosenbusch J.P.;
 RT "Crystal structures explain functional properties of two E. coli
 porins.";
 RL Nature 358:727-733(1992).
 RN [9]
 RP TOPOLOGY.
 RX MEDLINE-93172954; PubMed-7679770;
 RA Struyve M., Visser J., Adriaanse H., Benz R., Tommassen J.;
 RT "Topology of PhoE porin: the 'eyelet' region.";
 RL Mol. Microbiol. 7:131-140(1993).
 CC -I- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN E. COLI CELLS
 ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS
 PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
 PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
 SOLUTES.
 CC -I- SUBUNIT: HOMOTRIMER.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -I- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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 or send an email to license@sib-sib.ch)
 CC -----
 CC EMBL: V00316; CA23605.1; -;
 DR EMBL: D83536; BAA7910.1; -;
 DR EMBL: AE000132; AAC73345.1; -;
 DR EMBL: U70214; AAB08661.1; -;
 DR EMBL: X00786; CA23605.1; -;
 DR PIR: A03432; MMECPD.
 DR PDB: 1PHO; 3I-OCT-93.
 DR SWISS-2DPAGE: P02932; COLI.
 DR ECODBASE: B037.O; 6TH EDITION.
 DR EcoGene: EG10729; phoe.
 DR InterPro: IPR001702; -;
 DR InterPro: IPR001897; -;
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLIIPORIN.
 DR PRINTS: PR00183; ECOLIIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Outer membrane; Transmembrane; Porin; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 351
 FT MUTAGEN 351 351 F->Y,N,S,V: LESS RESISTANT TO TRYPSIN.

FT	STRAND	25	26
FT	STRAND	30	35
FT	STRAND	37	45
FT	STRAND	52	53
FT	STRAND	56	65
FT	STRAND	71	82
FT	TURN	87	88
FT	STRAND	93	104
FT	TURN	105	107
FT	STRAND	108	116
FT	TURN	119	119
FT	HELIX	120	123
FT	TURN	124	126
FT	TURN	140	141
FT	TURN	143	145
FT	STRAND	147	157
FT	TURN	159	162
FT	TURN	164	165
FT	STRAND	166	173
FT	STRAND	176	176
FT	TURN	182	183
FT	STRAND	185	185
FT	STRAND	188	197
FT	TURN	198	201
FT	STRAND	202	212
FT	HELIX	215	217
FT	TURN	218	219
FT	STRAND	227	239
FT	TURN	240	241
FT	STRAND	242	252
FT	STRAND	264	274
FT	STRAND	280	292
FT	STRAND	294	294
FT	TURN	295	297
FT	STRAND	298	298
FT	STRAND	301	313
FT	STRAND	318	327
FT	TURN	334	335
FT	STRAND	342	350
SO	SEQUENCE	351 AA; 38922 MW; 2492E362C030C9A CRC64;	

Query Match 56.8%; Score 1109; DB 1; Length 351;
 Best Local Similarity 58.3%; Pred. No. 4, 3e-70;
 Matches 217; Conservative 53; Mismatches 76; Indels 26; Gaps 9;

QY	1	MSKVTALLIPALLAAGAAHAEEVYKDKGKLDYKVDGLIHFSNKKVDGDTYMRIG	60
DB	1	MKSTALVVMGIVASASVQAAEYKDKGKLDYKVRAMHYMSDNASKDGQSYIRFG	60
QY	61	FGGETOVTOLGYGOWEYOIGNSAENEN-NSMTRVAFAGLKFQDVGSPDYGRNGVY	119
DB	61	FKGETOINDOLIGYRWMEAFPAKNKASPTAOKTKLALRGLKYLKDGSGFDYGRNIGALX	120
QY	120	DVTSMTDVLPEFGDTYG-SDNFMQGRGNFGATYRNTDFEGLVDGLNFAVOYQKNGNPS	178
DB	121	DVEAMTDMPEFGDSSAQTDNFMTRKASGLATYRNTDFEGLVDGLNLTLYQKNGNEN--	178
QY	179	GEGFTSGVTNNGRDALRQNGDVGSGITYDYBS-FCIGALISSKRTDAQNTAAIYKNG	236
DB	179	-----RDVYKQNGDDEGTSLSLTDFGSGDPAISGAYTNSDRTNDSNLSQSH-GTG	225
QY	237	DRAETVGLTKYDANNIYLAAYOTYTNATRVGSLGMANKAONFEVAVOYQDFGLRPSL	296
DB	226	KRAEMATGLKTDANNIYLAITYSETRKMTPIIG-GFAKTONFEVAVOYQDFGLRPSL	284
QY	297	AYLOSCKNMLGSGYDEDDILKYVDGATYTFNKNMSTVYDYKINLTD-DNOEFTRDAGINT	355
DB	285	GYVLSKGNKI-EGIGDEDLVNIDVGATYTFNKNMSAFDYKINQDSNKL-----NINN	339
QY	356	DNIVAGLYVQF 367	
DB	340	DDIVAVGMTYQF 351	

Search completed: September 25, 2001, 15:55:22
Job time: 121 sec

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Db      61 FKGETQVTDQLTGYGMEYQIQGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNRYGVVD 120
      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 180
      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 178
      181 GFTSGVTNNRGDRLRONGDVGSGITYDYEGFGIGAISSSKRTDQNTAAAYIGNDRAE 240
      179 ---EGMTNNGRELRONGDVGSGITYDYEGFGIGAISSSKRTDQNTAAAYIGNDRAE 235
      241 TYTGGLKYDANNIYLAQYQTYNATRVGSLGWANKAQNFEAFAVOYQFDFGLRPSLAYLQ 300
      236 TYTGGLKYDANNIYLAQYQTYNATRVGSLGWANKAQNFEAFAVOYQFDFGLRPSLAYLQ 295
      301 SKGKNL-----GRCYDEDEDILKYDVGATYTFNKNMSTYVDYKINLLDDNOFTDAGINTD 356
      296 SKGKNLGVINGRNYDEDILKYDVGATYTFNKNMSTYVDYKINLLDDNOFTDAGINTD 355
      357 NIYALGLVYQF 367
      356 NIYALGLVYQF 366

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RESULT 2
ID      09K597      PRELIMINARY;      PRT;      364 AA.
AC      09K597:
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      OUTER MEMBRANE PORIN C PRECURSOR.
GN      OMP.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Escherichia.
OX      NCBI_Taxid=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Low A.S., MacKenzie F.M., Gould I.M., Booth I.R.;
RT      "Parallel evolution of multi-resistant bacteria in a patient with
RT      recurrent septicemia: unique data that support the presence of
RT      separate protected environments."
RL      Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC      (BY SIMILARITY).
DR      EMBL; AJ295721; CAC01403.1; -.
DR      InterPro; IPR000504; -.
DR      InterPro; IPR001702; -.
DR      Pfam; PF00267; Gram-ve_porins; 1.
DR      PRINTS; PR00182; ECOLNEIPORIN.
DR      PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR      PROSITE; PS00030; RNP_1; UNKNOMN_1.
KW      Outer membrane; Porin; Signal; Transmembrane.
FT      SIGNAL 1 21
FT      CHAIN 1 21
FT      POTENTIAL.
SQ      SEQUENCE 364 AA; 40312 MW; 9B583F2C1344E31 CRC64;

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Query Match      87.5%; Score 1709.5; DB 2; Length 364;
Best Local Similarity 88.0%; Pred. No. 3.4e-113;
Matches 333; Conservative 14; Mismatches 27; Indels 3; Gaps 1;
      1 MKSKVLLALLIPALLAAGAAHAAEVYNNKDKNKLDTLGYKVDGLHYFSDNKVDQDQTYMRGLG 60
      1 MKKVVSLVLPALLVAGAAHAAEIYNNKDKNKLDTLGYKVDGLHYFSNDKSDGSKITMRGLG 60
      61 FKGETQVTDQLTGYGMEYQIQGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNRYGVVD 120
      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 180
      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 180

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Db      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 180
      181 GFTSGVTNNRGDRLRONGDVGSGITYDYEGFGIGAISSSKRTDQNTAAAYIGNDRAE 240
      181 GMT---TNGRDVFEONGDVGSGITYDYEGFGIGAISSSKRTDQNTTGLIGDRAE 237
      241 TYTGGLKYDANNIYLAQYQTYNATRVGSLGWANKAQNFEAFAVOYQFDFGLRPSLAYLQ 300
      238 TYTGGLKYDANNIYLAQYQTYNATRVGSLGWANKAQNFEAFAVOYQFDFGLRPSLAYLQ 297
      301 SKGKNLGRGYDEDEDILKYDVGATYTFNKNMSTYVDYKINLLDDNOFTDAGINTDNTA 360
      298 SKGKNLGRGYDEDEDILKYDVGATYTFNKNMSTYVDYKINLLDDNOFTDAGINTDNTA 357
      361 LGLVYQF 367
      358 LGLVYQF 364

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RESULT 3
ID      09K3E6      PRELIMINARY;      PRT;      378 AA.
AC      09K3E6:
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      OUTER MEMBRANE PROTEIN C PRECURSOR.
GN      OMP.
OS      Salmonella enterica subsp. enterica serovar Minnesota.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Salmonella.
OX      NCBI_Taxid=70803;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN-SF111;
RA      Zimmermann H., Wassenaar T.M., Laubenthaler-Preusse H., Pety F.,
RA      Loos M.;
RL      Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC      (BY SIMILARITY).
DR      EMBL; Y15844; CAB96613.1; -.
DR      InterPro; IPR000504; -.
DR      InterPro; IPR001702; -.
DR      Pfam; PF00267; Gram-ve_porins; 1.
DR      PRINTS; PR00182; ECOLNEIPORIN.
DR      PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR      PROSITE; PS00030; RNP_1; UNKNOMN_1.
KW      Outer membrane; Porin; Signal; Transmembrane.
FT      SIGNAL 1 21
FT      CHAIN 1 21
FT      POTENTIAL.
SQ      SEQUENCE 378 AA; 41269 MW; 254524EB9EC3849C CRC64;

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Query Match      78.6%; Score 1534.5; DB 2; Length 378;
Best Local Similarity 77.1%; Pred. No. 8e-101;
Matches 296; Conservative 25; Mismatches 40; Indels 23; Gaps 5;
      1 MKSKVLLALLIPALLAAGAAHAAEVYNNKDKNKLDTLGYKVDGLHYFSDNKVDQDQTYMRGLG 60
      1 MKKVVSLVLPALLVAGAAHAAEIYNNKDKNKLDTLGYKVDGLHYFSNDKSDGSKITMRGLG 60
      61 FKGETQVTDQLTGYGMEYQIQGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNRYGVVD 120
      61 FKGETQVTDQLTGYGMEYQIQGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNRYGVVD 120
      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 180
      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 180
      121 VTSWTDVLPFEGGDTYGSNFMQGRNGFATYRNTDFEGLVLDGLNFAVOYQGRNGNPSGE 180
      181 GFTSGVTNNRGDRLRONGDVGSGITYDYEGFGIGAISSSKRTDQNTAAAYIGNDRAE 240
      181 -----NDGGRSLNONGDVGSGITYDYEGFGIGAISSSKRTDQNTDADRLYNG 234

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QY	237	DRAEYVYGGLEYDANNNTYLAQYQYTNATFVG-----SLGMAKKKQNFPAVAQYQ	287
Db	235	DRAYVYVGGLEYDANNNTYLLAQYISQTNATNFTGTSNGNKKSDSTGFANKKQNFPAVAQYQ	294
QY	288	FDFGLRPSLAVTQSKGNKILGRG---YDDEDILKXYVDVGATYYFNKMNSTYVDKINLLD	343
Db	295	FDFGLRPSVAVTQSKGKDINSNGYASTSGDDDIVAYVDVGATYYFNKMNSTYVDKINLLD	354
QY	344	DNCFTRDAGINTDNIVALGLVYQF	367
Db	355	KDNFTRDAGINTDNIVALGLVYQF	378

RESULT	4			
ID	085030	PRELIMINARY:	PRT:	377 AA.
AC	085030;			
DT	01-NOV-1998 (TREMblrel. 08, Created)			
DT	01-NOV-1998 (TREMblrel. 08, Last sequence update)			
DT	01-MAR-2001 (TREMblrel. 16, Last annotation update)			
DE	PORIN OMPN.			
GN	OMP _N .			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562;			
RN	1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BE (BL21) ;			
RX	MEDLINE=98317278; PubMed=9642192;			
RA	Pillipov A., Phale P.S., Koehnlik R., Widmer C., Rosenbusch J.P. ;			
RT	"Identification and Characterization of two quiescent porlin genes			
RT	mpc and omp _N in Escherichia coli BE." ;			
RL	J. Bacteriol. 180:3388-3392(1998).			
DR	EMBL, AF035618; AAC38644.1; -.			
DR	HSSP: P02931; IGFN.			
DR	InterPro: IPR00408; -.			
DR	InterPro: IPR001702; -.			
DR	Pfam: PF00267; Gram-ve.porins. 1.			
DR	PRINTS: PR00182; ECOLNIPORIN.			
DR	PROSITE: PS00626; RCCL_2; UNKNOWN_1.			
Q	SEQUENCE 377 AA: 41336 MW; FFD6B91AB2C10F8C CRC64;			

	Query Match	66.4%;	Score 1296;	DB 2;	Length 377;
	Best Local Similarity	68.1%;	Pred. No.5.5e-84;		
	Matches 262;	Conservative 36;	Mismatches 61;	Indels 26;	Gaps 10;
QY	1	MKSVYLLALLIPALLAAGAAHAEEVYNNKQGNKLDLTGKVDGLHYFSDNKNKVDSDQTYMRIG	60		
Db	1	MKSVYLLALLIPALLAAGAAHAEEVYNNKQGNKLDLTGKVDGLHYFSDNKSABDQSGTARIG	60		
QY	61	EKGETQVTDLTGTQGWMEYIQGNSAE--NENNSWTRVAFAGLKEFDVGSFEDYGRNRYGVY	119		
Db	61	EKGETQINDQLTGTQGWMEYNIQANTTESSKNSQSWTRIFAGLKEFDYGSFEDYGRNRYGVY	120		
QY	120	DVTSWTDVLPFEGDDTY--GSDNFMQGRNFGATYNTDFEGLVDGLNPAVOYQSGKNNS	178		
Db	121	DIEGWTDLPEFGDSDSYTNADNFMFGNAGVATYRNTDFEGLVNLNPAVOYQGNNT---	176		
QY	179	GEGETSGV--TNNGRDALRONGDVGSGSITVDY--EGFGTGAISSSKPRDAQ--NTAAVI	233		
Db	177	EGASNGOEGEINNCRDVAHENGDMGLSTTYDGLGGEFSAAGAYTSSDRINDQVNHATA--	233		
QY	234	GNDRAEYTYTGLKYDANNITLAAYTOTYATNATRVSLGW--ANKAONEEAAVOYQOFDFG	291		
Db	234	GGKADAMWTAGLKYDANNITLATATMYSETRRMTPFGSDSDYAVANTQONEEVAAYQOFDFG	292		
QY	292	LRPSLATYQSGKNL-----GGGYDDEDLKTVVDGATYYFNKKNSTYYDYKINLLD	343		
Db	293	LRPASVETMSGGRDLHAAGADNPNPVGVDKDLVYKADYADGATYYFNKKNSTYYDYKINLLD	352		

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QY      344 -DNQFTRDAGINTDNIVALGLVYQF 367
          | : | ||:|:| | | | | | | | |
Db      353 EDDSFYTAGISTDDIVALGLVYQF 377
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RESULT	5			
ID	087754	PRELIMINARY;	PRT:	374 AA.
AC	087754;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)			
DE	OMPk37 PORIN PRECURSOR.			
GN	OMPk37.			
OS	Klebsiella pneumoniae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Klebsiella.			
OX	NCBI_TaxID=573;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SB8;			
RA	Domenech-Sanchez A., Hernandez-Alles S., Martinez-Martinez L.,			
RA	Benedi V.J., Alberti S.;			
RT	"Identification and characterization of a novel porin of Klebsiella			
RT	pneumoniae: its role in beta-lactam antibiotics resistance.";			
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: A011502; GSA09666.1; -;			
DR	HSSP: Q48473; IOSM.			
DR	InterPro: IPR000408; -;			
DR	InterPro: IPR001702; -;			
DR	Pfam: PF00267; Gram-ve.porins; 1.			
DR	PRINTS: PR00182; ECOLNEIPORIN.			
DR	PROSITE: PS00626; RC01_2; UNKNOWN_1.			
KW	SIGNAL.			
FT	SIGNAL. 1 21	POTENTIAL.		
FT	CHAIN 22 374	OMPk37 PORIN.		
Q	SEQUENCE 374 AA; 41612 MW; B66DF0D74A1A169B CRC64;			

[illegible]

RESULT 6

09K3E7 PRELIMINARY; PRT; 363 AA.
 ID 09K3E7
 AC 09K3E7
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
 DE OUTER MEMBRANE PROTEIN FX PRECURSOR.
 GN OMPF.
 OS Salmonella enterica subsp. enterica serovar Minnesota.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxId=70803;
 OX NCBI_TaxId=70803;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SE111;
 RA Zimmerman H., Wassenaar T.M., Laubenheimer-Preusse H., Petry F.,
 RA Loois M.,
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y15843; CAB9614.1; -.
 DR InterPro: IPR001702; -.
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLNEIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; UNKNOWN_1.
 DR SIGNAL.
 KW SIGNAL.
 FT CHAIN 23 363 OUTER MEMBRANE PROTEIN FX.
 FT SEQUENCE 363 AA; 40090 MW; F5058DDEA516859 CRC64;
 SQ SEQUENCE

Query Match 52.5%; Score 1025.5; DB 2; Length 363;
 Best local Similarity 53.2%; Pred. No. 6.5e-65;
 Matches 201; Conservative 60; Mismatches 90; Indels 27; Gaps 7;

QY 1 MKKVALILPALLAAGAAHAAYNNKDKLKYVGLHFPDNDK--VDDQDTYMR 59
 DB 2 MKKKIILAAVPAALAAATANAELTYNDGKLDLYGKAGRHAWTTTGGSKNDDQTAQI 61
 QY 60 GFGKGTQVTDLTGYGQWEYIOGNSAENE--NNSWTRVAFAGLKTQDVGSFPGYGRNYGV 117
 DB 62 GFGKGTQVTDLTGYGQWEYRTKADRAEGQNSNLVRLAFAGLKYAEVGSIDYGRNYGI 121
 QY 118 VYVYSTVDLPEFGDITYG---SDNFMQQRNGFATYRTDFFGLVDGLNFPAVOYQGN 174
 DB 122 VYVYESTVDAPYFSGTGWGAYTDMYMSRAGLLTYRNSDFEGLVDGLSFQIOYQGN 181
 QY 175 GNDSGEGFTSGVYNNGRDALRONGDVGSGITDYDEFGAIGSSSKRTDQNTAAYIG 234
 DB 182 -----QDNHSINSQNGDVGVTMAEFDGFTAAYSNSKRTINDQDRD--G 226
 QY 235 NGDRAETTYGGLKYDANNITVLAQYQTNYNA-----TRVSGLGMANKQNEFAVAQYQFD 289
 DB 227 NGDRAESMAVAGAYDANNVYLAAYVETRMMSIVENTVTQTEAMANKTQULEVVAQYQFD 286
 QY 290 FGURPSLAIYQSGKNGKRGYDDEDLIKYDVATYFENKMSYVDYKINLDDNQFTR 349
 DB 287 FGURPAISYVQSGKQNGAGSADLAKYIQAGATYFENKMSVWVDYRPNLDDENDYS- 345
 QY 350 DAGINTDNVALGLVYQF 367
 DB 346 SSTYGTDVQAAGVITYQF 363

RESULT 7
 09RAW3 PRELIMINARY; PRT; 333 AA.
 ID 09RAW3
 AC 09RAW3
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
 DE PHOSPHATE PORIN (FRAGMENT).
 GN PHOE.
 OS Klebsiella pneumoniae (subsp. ozaenae).
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.
 OX NCBI_TaxId=574;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=I436;
 RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Sriprakash K.S.,
 RA Kemp D.J.,
 RT "Phylogenetic analysis of Calymmatobacterium granulomatis."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY)
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
 CC (BY SIMILARITY).
 CC EMBL: AF009229; AAD21517.1; -.
 DR HSSP: P02932; LPHO.
 DR InterPro: IPR001702; -.
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLNEIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Outer membrane; Porin; Signal; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 333 333
 SQ SEQUENCE 333 AA; 36839 MW; 68AF347207770ABA CRC64;

Query Match 52.2%; Score 1018.5; DB 2; Length 333;
 Best local Similarity 56.5%; Pred. No. 1.8e-64;
 Matches 200; Conservative 53; Mismatches 76; Indels 25; Gaps 8;

QY 8 LILPALLAAGAAHAAYNNKDKLKYVGLHFPDNDKVDVQDTYMRIGKGTQY 67
 DB 1 LMMGVASATQAOAAAYNNKANKLDVYGKIKAMHFSYDSDSKDQTYVRFQIKGTQI 60
 QY 68 TDLTGYGQWEYIOGNSAENNSWTRVAFAGLKTQDVGSFPGYGRNYGVYVDTSMPTQY 127
 DB 61 NDULTYGRKESEFSGNKTESDSQKTRLAFAVGLKNTGSPFYGNLGLVDYEAWTQM 120
 QY 128 LPEFGDITYG--SDNFMQQRNGFATYRTDFFGLVDGLNFPAVOYQGNPNSGEGFTSGV 186
 DB 121 LPEFGDSSAQDTNFMFKRASGLATYRTDFFGLVDGLDLTLQYQCK----- 167
 QY 187 TNGGRALRONGDVGSGSTIYDEG--FGLGGAIGSSSKRTDQNTAAYIGNDRAETTYG 244
 DB 168 -NGEGRAKKQNGDVGSTSYDFGSDFAVASAYTSSDRTDQNLAR--GQGSKAEMAT 225
 QY 245 GLKYDANNITVLAQYQTNAATRVGSLGMANKQNEFAVAQYQFDGLPSLAIYQSGK 304
 DB 226 GLKYDANNITVLAQYQETRMPTI--SGFRANKQNEFAVAQYQFDGLPSLGIYQSGK 284
 QY 305 NLGRGYDDEDLIKYDVATYFENKMSYVDYKIN--LDDNQFTRDAGINTDN 357
 DB 285 DI-EGVGSDELVYIDVGLTYFENKMSNAFVDYKINQLKSDNKL---GINDDD 333

RESULT 8
 09RAW2 PRELIMINARY; PRT; 333 AA.
 ID 09RAW2
 AC 09RAW2
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
 DE PHOSPHATE PORIN (FRAGMENT).
 GN PHOE.
 OS Klebsiella pneumoniae subsp. rhinoscleromatis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 NCBI_TaxId=39831;
 OX NCBI_TaxId=39831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC5046;
 RX MEDLINE=20023050; PubMed=1055350;
 RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Sriprakash K.S.,
 RA Kemp D.J.,
 RT "Phylogenetic evidence for reclassification of Calymmatobacterium


```
Db 62 GFGGQETQINFDLFGQWEMERTKADRAEGBOQNSNLVRLAFAGLKAVEGSDYGRNYGI 121
118 YVYVSTWTDVLPREGGDTYG---SDNPMOQRGNFAGATYRTDFFGLVDGLNFAVOYQGN 174
122 YVYVSTWTDVLPREGGDTYG---SDNPMOQRGNFAGATYRTDFFGLVDGLNFAVOYQGN 181
175 GNSGEGFTSGVYNNGRDARONGDVGSGITYDEFGIGGAISSSKRTDAONTAAYIG 234
182 -----QDNHSINSQNGDGYGTMAIEFDGFGYTAAYNSKRTINDODR- G 226
QY 235 NGDRAETTYGGLKYDANNITLAAQYOTQYNA-----TRVSLGMANKAONEFAVAOYQFD 289
227 NGDRAESWAGAKAYDANNVYLAAYETRNMSIYENTVDTVEAKNTQMLEVAOYQFD 286
QY 290 FGLRPLSLAYLOSCKNKGRIYDDEDLIKYVDGATYFNKMSYVDYKINLDDNQFTR 349
287 FGLRPLSLAYLOSCKNKGRIYDDEDLIKYVDGATYFNKMSYVDYKINLDDNQFTR 345
Db 350 DAGINTDNIVALTGLV 364
QY 346 SSYVGTDGDAAGVIV 360
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RESULT 11
Q9RR59 PRELIMINARY: PRT; 333 AA.
AC 09RR59:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE PHOSPHATE PORIN (FRAGMENT).
GN PHOE.
OS Calymmatobacterium granulomatis
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Calymmatobacterium.
OX NCBI_TaxID=39824;
RP SEQUENCE FROM N.A.
RX MEDLINE-20023050; PubMed-10555350;
RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Sripaksh K.S.,
  Kemp D.J.,
  Phylogenetic evidence for reclassification of Calymmatobacterium
  granulomatis as Klebsiella granulomatis comb. nov.*;
RC Int. J. Syst. Bacteriol. 49:1695-1700(1999).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
  (BY SIMILARITY).
DR EMBL: AF009231; AAD21519.1; -.
DR HSSP: P02932; IPHO.
DR InterPro: IPR001702; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLNEIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Porin; Signal; Transmembrane.
FT NON_TER 1
FT TER 333
SQ SEQUENCE 333 AA; 36786 MW; 7CEA2F68B998BB0A CRC64;
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Query Match 51.7%; Score 1010.5; DB 2; Length 333;
Best Local Similarity 56.2%; Pred. No. 6.6e-64;
Matches 199; Conservative 53; Mismatches 77; Indels 25; Gaps 8;
QY 8 LILPALLAAGAAHAEEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQTYRRLGKSETQV 67
1 LMMGVASTATQAAEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQTYRRLGKSETQV 60
Db 1 LMMGVASTATQAAEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQTYRRLGKSETQV 60
QY 68 TQOLTGYQWMEYQIOGNSAENNNNSWTRVAFAGLKFQDVGSGYGRNYGVYVDTSMYTV 127
1 LMMGVASTATQAAEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQTYRRLGKSETQV 60
Db 61 NNDLTGYGWESFSGNKNKESDSSQKTRLAFAGVKLKNGSPFYGNLGLALYVEMANTDM 120
QY 128 LPBEGGDTYG-SDNPMOQRGNFAGATYRTDFFGLVDGLNFAVOYQGNPSEGGFTSGV 186
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Db 121 FPEGGDSSAQTDNFMTRKASGLATYRTDFFGLVDGLDITLQYQK----- 167
187 TNGRDLALRQNGGCVGSITYDEG--FGIGGAISSSKRTDAONTAAYIGNDRATYTG 244
168 -NEGCEARKQNGDVGSTSLYDEGSDFAVSAVYTSDDRTNDONLLAR-GQGSKAAMAT 225
QY 245 GLKYDANNITLAAQYOTQYNAATVSGLSGMANKAONEFAVAOYQFDGRLPSLAYLOSCK 304
226 GLKYDANNITLAAQYOTQYNAATVSGLSGMANKAONEFAVAOYQFDGRLPSLAYLOSCK 284
Db 305 NIGRGYDDEDILKYVDGATYFNKMSYVDYKINLDDNQFTRDAGINTDN 357
285 DI-EGVSEDLVNYIDVGLTYFNKMSYVDYKINLDDNQFTRDAGINTDN 333
```

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RESULT 12
087753 PRELIMINARY: PRT; 359 AA.
AC 087753:
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE OMPK35 PORIN PRECURSOR.
GN OMPK35.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RP SEQUENCE FROM N.A.
RX STRAIN-KT755;
RA Hernandez-Alles S.;
  Thesis (1998): Universidad de les Illes Balears, Valencia, Spain.
DR EMBL: AJ011501; CA09665.1; -.
DR HSSP: P02931; IGEN.
DR InterPro: IPR001702; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLNEIPORIN.
KW SIGNAL.
FT CHAIN 1 22 POTENTIAL.
FT SIGNAL 1 22 OMPK35 PORIN.
FT CHAIN 23 359
SQ SEQUENCE 359 AA; 39510 MW; 12D518340058E5BB CRC64;
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Query Match 51.7%; Score 1009.5; DB 2; Length 359;
Best Local Similarity 53.5%; Pred. No. 8.6e-64;
Matches 200; Conservative 54; Mismatches 97; Indels 23; Gaps 6;
QY 1 MKSKVALLIPALLAAGAAHAEEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQ- TYMRL 59
2 MKRNILAVYIPALVAGAAHAEEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQ- TYMRL 61
Db 2 MKRNILAVYIPALVAGAAHAEEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQ- TYMRL 61
QY 60 GKEGFTQVTDLTGYQWMEYQIOGNSAENNNNSWTRVAFAGLKFQDVGSGYGRNYGVY 119
1 LMMGVASTATQAAEVYNNKDKKLDLYGKVDGLHFPSDNKDVDDQTYRRLGKSETQV 60
Db 62 GKEGFTQVTDLTGYQWMEYQIOGNSAENNNNSWTRVAFAGLKFQDVGSGYGRNYGVY 121
QY 120 DYTSMWTDVLPREGGDTYG-SDNPMOQRGNFAGATYRTDFFGLVDGLNFAVOYQGNNGNS 178
120 DYTSMWTDVLPREGGDTYG-SDNPMOQRGNFAGATYRTDFFGLVDGLNFAVOYQGNNGNS 178
Db 122 DVEAATDMLVEMGGDGMWNTDNYMTGRNGVATYRNSDFGLVDGLSLFALQYQGNK---- 177
QY 179 GEGFTSGVYNNGRDARONGDVGSGITYDE- GFGIGGAISSSKRTDAONTAAYIGNCD 237
179 GEGFTSGVYNNGRDARONGDVGSGITYDE- GFGIGGAISSSKRTDAONTAAYIGNCD 237
Db 178 -----DHRALRKQNGDGFSTAATYAFNGIALSAGYSSSRNSRVQKAD---GNCD 225
QY 238 RAETTYGGLKYDANNITLAAQYOTQYNAATVSGLSGMANKAONEFAVAOYQFDGRLPSLA 297
238 RAETTYGGLKYDANNITLAAQYOTQYNAATVSGLSGMANKAONEFAVAOYQFDGRLPSLA 297
Db 226 KAEAMATSAKYDANNITLAAQYOTQYNAATVSGLSGMANKAONEFAVAOYQFDGRLPSLA 285
QY 298 YLOSCKKNL-----GREGYDDEDILKYVDGATYFNKMSYVDYKINLDDNQFTRDAGI 353
298 YLOSCKKNL-----GREGYDDEDILKYVDGATYFNKMSYVDYKINLDDNQFTRDAGI 353
Db 286 YVOTKGRDLOSRAFGSGGDADLVKTIENGVTWYFNKMSYVDYKINLDDNQFTRDAGI 345
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OY 354 NTDNIALGLVYQF 367
 DB 346 ATDDQAAVGIVQF 359

RESULT 13

O9EXH8 PRELIMINARY; PRT; 315 AA.
 AC O9EXH8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE OMPK35 PROTEIN PRECURSOR.
 GN OMPK35.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxId=573;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=103624;
 RA Crowley B., Benedi V.J., Domenech-Sanchez A.;
 RT "Expression of altered ompK35 porin and SHV-2 beta-lactamase in
 Klebsiella pneumoniae results in cephalosporins and carbapenems
 resistance.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ303057; CAC18650.1; -
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 315 OMPK35 PROTEIN.
 SO SEQUENCE 315 AA; 34420 MW; F4574838475D8CA CRC64;

Query Match 44.2%; Score 862.5; DB 2; Length 315;
 Best Local Similarity 52.9%; Pred. No. 1.7e-53;
 Matches 174; Conservative 47; Mismatches 85; Indels 23; Gaps 6;

OY 1 MRSKVLALIPALLAAGAAHAEEVYNKDKNKLDYGVKVDLHYFSDNKKDVGDDQ-TYMRL 59
 DB 2 MKNITLAVIPALLVGAANAALYNNKNGKLDYGVKMEHWTNMGDTSDDTYARI 61
 OY 60 GFGEGTQVTDLTGYGMEYQIQGNSAENENN-SWTRVAFGLKFDQVGSFDYGRNTGVY 119
 DB 62 GLGGETQINDLTGYGMEYQIQGNSAENENN-SWTRVAFGLKFDQVGSFDYGRNTGVY 121
 OY 120 DVATSWTDVLPFGGDTYG-SDNFMQORGNFGATYRNTDFGLVGLFAVQYOGKNGNPS 178
 DB 122 DVPAALDMLVEMGGDGNNTDNTMTGRTNGVATYRNSDFGLVGLSFLQYOGKN--- 177
 OY 179 GEGFTSGVTNNGRDALRONGDVGGSITYDY- GFGIGGAISSSKRTDAQNTAAYIGNGD 237
 DB 178 -----DHDRAIRKQNDGFSFATYAFDNGIALSAGYSSNRNSVDQKAD--GNGD 225
 OY 238 RAETTYGGLKYDANNITYLAQYQTYNATRVGSLGNANKRQNEFAVAQYQFDPGLRPSLA 297
 DB 226 KAAAMATSAAYDANNITYLAAYVSYQTYNMTPEEDNHFAKTYQNEAVVQYQFDEGLRPSI 285
 OY 298 YLQSKGKNL-----GRGYDEDILKYDVVG 322
 DB 286 YVOTKRGDLOSRAFGSGADLVKTYIEVG 314

RESULT 14

O9ZC71 PRELIMINARY; PRT; 315 AA.
 AC O9ZC71;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.

OX NCBI_TaxId=632;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=6/69;
 RA Buchrieser C., Rusniok C., Couve E., Frangeul L., Billault A.,
 RA Kunst F., Carniel E., Glaser P.;
 RT "DNA sequence of the 102 kbases unstable region of Yersinia pestis.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL031866; CAA21336.1; -
 DR HSSP: P02931; 1GFN.
 DR InterPro: IPR001702; -
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLNEIPORIN.
 SO SEQUENCE 315 AA; 34304 MW; D32FB91828EDA17A CRC64;

Query Match 37.5%; Score 732; DB 2; Length 315;
 Best Local Similarity 51.5%; Pred. No. 2.8e-44;
 Matches 158; Conservative 40; Mismatches 83; Indels 26; Gaps 9;

OY 1 MRSKVLALIPALLAAGAAHAEEVYNKDKNKLDYGVKVDLHYFSDNKKDVGDDQF 55
 DB 1 MKNITLAVIPALLVGAANAALYNNKNGKLDYGVKMEHWTNMGDTSDDTYARI 61
 OY 56 YMRIGFEGTQVTDLTGYGMEYQIQGNSAENENN-SWTRVAFGLKFDQVGSFDYGR 113
 DB 54 YVRIGFEGTQVTDLTGYGMEYQIQGNSAENENN-SWTRVAFGLKFDQVGSFDYGR 113
 OY 114 NYGVYVYVTWTDVLPFGGDTY-GSDNFMQORGNFGATYRNTDFGLVGLFAVQYOG 172
 DB 114 NYGVYVYVTWTDVLPFGGDTY-GSDNFMQORGNFGATYRNTDFGLVGLFAVQYOG 173
 OY 173 KGNPSCGFTSGVTNNGRDALRONGDVGGSITY-DYEGFGI--GGAISSSKRTDAQNT 229
 DB 174 RNED-----GDVTRNERSIQKANGDGFGLSFNYQIQGSGVFAAYSSNNTBEQKE 226
 OY 230 AAYIGNGRAETTYGGLKYDANNITYLAQYQTYNATRVGSLGNANKRQNEFAVAQYQF 289
 DB 227 LVNSAAGDKQAAMATGLKYDANNITYLAAYVSYQTYNMTPEEDNHFAKTYQNEAVVQYQF 285
 OY 290 FGLRPSL 296
 DB 286 NGIRPSL 292

RESULT 15

O52641 PRELIMINARY; PRT; 130 AA.
 AC O52641;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE OMPK (FRAGMENT).
 GN OMPK.
 OS Rahnelia aquatilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Rahnelia.
 OX NCBI_TaxId=34038;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=CF3;
 RA Achouak W., de Mot R., Heulin T.;
 RL FEMS Microbiol. Ecol. 0:0-0(0).
 DR EMBL: U17430; AAA56871.1; -
 DR HSSP: P09878; 1TIV.
 DR InterPro: IPR001702; -
 DR Pfam: PF00267; Gram-ve_porins; 1.
 FT NON_TER 1 1
 FT NON_TER 130 130
 SO SEQUENCE 130 AA; 14510 MW; DB6A341744A48EF5 CRC64;

Query Match 26.5%; Score 518.5; DB 2; Length 130;

